

# Fully automatic analysis of DNA microarray images

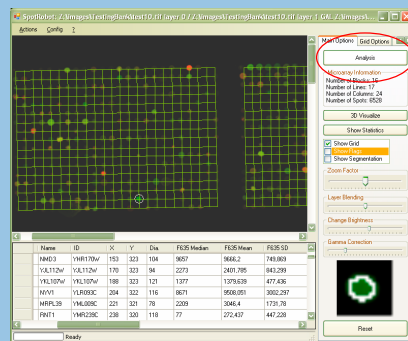
S.Mitterhuber, B.Petersch, O.Serrano. *Advanced Computer Vision GmbH - ACV, Vienna, Austria, [www.acv.ac.at](http://www.acv.ac.at)*

ADVANCED COMPUTER VISION

An Enterprise of the Austrian Research Centers

## Abstract

During the last years, the advent and rapid development of DNA microarray techniques has revolutionized genetic research in life sciences. We are presenting a new **stand-alone software** for fully automated analysis of microarray images. It employs a number of **novel image processing algorithms** for grid detection and spot segmentation which assure high calculation **speed** and **accuracy**. The software can be run using a self-explanatory **graphical user interface (GUI)** or from the **command line** which gives additional flexibility and allows integration into larger microarray analysis frameworks. **Batches of images** as well as **single images** can be processed. The main benefits of this software over existing ones are its **extremely easy handling** (no user interaction required), the fast and robust gridding, the flexible free form spot segmentation and its multiple usage scenarios. We present examples of the performance of the proposed algorithms on real-world microarray images with heavy noise and artefacts.



## Introduction

Microarray image analysis software has to be

- easy to operate (minimum user input)
- fully automatic
- fast, robust and flexible
- affordable

We present a new software tool which only requires image location(s) and GenePix Array List file(s) as input, works fully automatic and achieves efficiency and robustness through a number of novel image processing algorithms.

## Methods

The proposed microarray image analysis chain consists of the following steps:

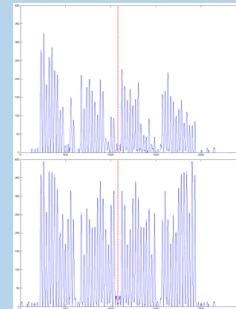
- Automatic **layer registration** (for multilayer experiments)
- **Pre-processing** (deals with spots brighter or darker than the background)
- Automatic **grid angle** determination based on Radon Transform (RT) projections [1]
- Fully automatic **Gridding**
- **Spot segmentation**
- Calculation of **spot qualities & statistical analysis**

### Symmetry Exploitation<sup>1</sup>

DNA microarray grid layouts exhibit symmetry which can be detected. Our algorithm performs

- detection of **symmetry axis** in RT-profiles,
- **enhancement of profiles**, and
- **peak detection**,

leading to a more **robust grid detection**.

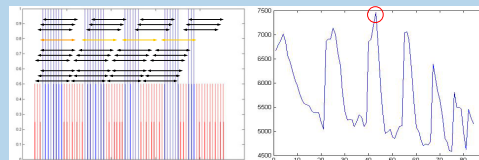


### Grid Reconstruction<sup>1</sup>

Information about the **block structure** can be read from a GAL file.

Our gridding algorithm automatically

- calculates the **grid constants** via auto-correlation of the RT-profiles,
- performs a **smart reconstruction algorithm** considering all possible grid positions, and
- determines the correct one based on a **quality criterion**.



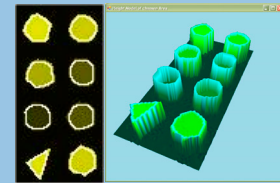
### Spot Segmentation<sup>1</sup>

Manual segmentation of DNA spots is a tedious task. Our algorithm **automatically segments spots of arbitrary shape** using distance calculation on image manifolds [2] combined with K-means clustering [3]. A possibility for **3D visualization** is provided.

### Graphical User Interface

The operation of the GUI is extremely easy:

- Load the images & GAL file
- Press "Analysis"
- Browse the results



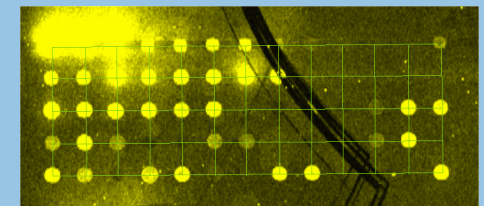
The spot signal and other statistical results are output to a file following the GenePix Result format. The segmentation results are saved as JPG images.

### Command Line Tool

- Alternative to GUI operation mode for both single image and batch processing;
- allows integration into other analysis frameworks and client-server architecture.

## Results

Due to the use of Intel's IPP functions and efficient implementations of all algorithms, processing time for an 11 megapixel 2-layer image ( $\sim 10^4$  spots) is as low as 60s on a P4 3.6GHz CPU with 2GB RAM. The distance-based spot segmentation adapts to arbitrary spot shapes and the gridding is very robust, even in the presence of substantial noise and image artefacts.



## Conclusions

We have presented a new software tool for **fully automatic analysis of DNA microarray images** which employs novel image processing algorithms and thus allows for **robust grid detection**, **adaptive spot segmentation** and **efficient data processing**. The graphical user interface and command line tool provide easy handling and flexibility in the choice of application scenarios.

**References**  
[1] N. Brande, H. Bischof, H. Lapp: Generic and robust approach for the analysis of spot array images; in Proc of SPIE: Microarrays: Optical Technologies and Informatics; vol. 4266; pp. 1-12; 2001.  
[2] M. W. Jones, A. Baerentzen, M. Sramek: 3D Distance Fields: A Survey of Techniques and Applications; in IEEE Trans Vis Comput Graph; vol. 12; no. 4; pp. 581-599; 2006.  
[3] A. K. Jain, R. C. Dubes: Clustering Methods and Algorithms; Algorithms For Clustering Data; pp. 55-142; Prentice-Hall; 1988

**Acknowledgment**  
We would like to thank Christa Nihammer, Silvia Fuch, Levente Bodrosy and Klemens Vierlinger from the Austrian Research Centers Seibersdorf for valuable discussions and feedback.