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FACULTY OF COMPUTER SCIENCE AND AUTOMATION

COMPUTER SCIENCE MEETS AUTOMATION

VOLUME II

Session 6 - Environmental Systems: Management and Optimisation

Session 7 - New Methods and Technologies for Medicine and Biology

Session 8 - Embedded System Design and Application

Session 9 - Image Processing, Image Analysis and Computer Vision

Session 10 - Mobile Communications

Session 11 - Education in Computer Science and Automation

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Preface

Dear Participants,

Confronted with the ever-increasing complexity of technical processes and the growing demands on their efficiency, security and flexibility, the scientific world needs to establish new methods of engineering design and new methods of systems operation. The factors likely to affect the design of the smart systems of the future will doubtless include the following:

- As computational costs decrease, it will be possible to apply more complex algorithms, even in real time. These algorithms will take into account system nonlinearities or provide online optimisation of the system's performance.
- New fields of application will be addressed. Interest is now being expressed, beyond that in "classical" technical systems and processes, in environmental systems or medical and bioengineering applications.
- The boundaries between software and hardware design are being eroded. New design methods will include co-design of software and hardware and even of sensor and actuator components.
- Automation will not only replace human operators but will assist, support and supervise humans so that their work is safe and even more effective.
- Networked systems or swarms will be crucial, requiring improvement of the communication within them and study of how their behaviour can be made globally consistent.
- The issues of security and safety, not only during the operation of systems but also in the course of their design, will continue to increase in importance.

The title "Computer Science meets Automation", borne by the 52nd International Scientific Colloquium (IWK) at the Technische Universität Ilmenau, Germany, expresses the desire of scientists and engineers to rise to these challenges, cooperating closely on innovative methods in the two disciplines of computer science and automation.

The IWK has a long tradition going back as far as 1953. In the years before 1989, a major function of the colloquium was to bring together scientists from both sides of the Iron Curtain. Naturally, bonds were also deepened between the countries from the East. Today, the objective of the colloquium is still to bring researchers together. They come from the eastern and western member states of the European Union, and, indeed, from all over the world. All who wish to share their ideas on the points where "Computer Science meets Automation" are addressed by this colloquium at the Technische Universität Ilmenau.

All the University's Faculties have joined forces to ensure that nothing is left out. Control engineering, information science, cybernetics, communication technology and systems engineering – for all of these and their applications (ranging from biological systems to heavy engineering), the issues are being covered.

Together with all the organizers I should like to thank you for your contributions to the conference, ensuring, as they do, a most interesting colloquium programme of an interdisciplinary nature.
I am looking forward to an inspiring colloquium. It promises to be a fine platform for you to present your research, to address new concepts and to meet colleagues in Ilmenau.

Professor Peter Scharff
Rector, TU Ilmenau

Professor Christoph Ament
Head of Organisation

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52nd Internationales Wissenschaftliches Kolloquium
Technische Universität Ilmenau
10 – 13 September 2007

U. Knauer / R. Stein / B. Meffert

Detection of Opened Brood Cells at an Early Stage

ABSTRACT

We present an algorithm for an early detection of the uncapping process of honeybee brood cells. It is a challenging problem, because the appearance of openings varies highly and the combs surface is crowded by bees.
The approach consists of two steps, segmentation of the image and analyzing the segments to give a report about openings.

INTRODUCTION

One of the biggest threats for the native honeybee *Apis melifera* is the mite *Varroa destructor* [1]. A promising approach to block the mites is the rearing of resistant bees. Therefore, current research in the field of apiculture focuses on the genetic selection of hygienic bees [2]. The selection of hygienic bees requires a time consuming observation of the combs. Processing all the material that is typically recorded for a period of one week (24 hours a day) requires at least twice the time for analysis by a human expert. Details on this procedure and proposals for acceleration by image processing techniques can be found in [3,4].

To summarize previous work, the identification of hygienic bees is always guided by the search for brood cells which have been uncapped by such bees. Only if openings can be detected as early as possible (see Fig. 1) the identification of hygienic bees will be improved. In this paper we present an algorithm to achieve a reliable early detection in cluttered images.

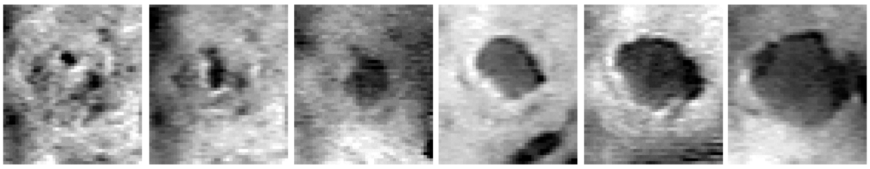


Fig. 1. Contrast-enhanced images of a brood cell. Early detection (state at the most left picture) is required.

The paper is structured as follows. First, we describe the preprocessing and segmentation of images. Next, a classifier for the detection of openings and first results are presented. Finally, we show the limitations of the approach and outline future work.

PREPROCESSING OF IMAGES

Fig. 2 gives an impression how the recordings from the observational beehive look like. A two step prescreening is applied to extract non-occluded images of each brood cell (i.e. as shown in Fig.1) for analysis. A survey on the performance of different algorithms on this problem and our final choice of the classifiers are provided in [4].

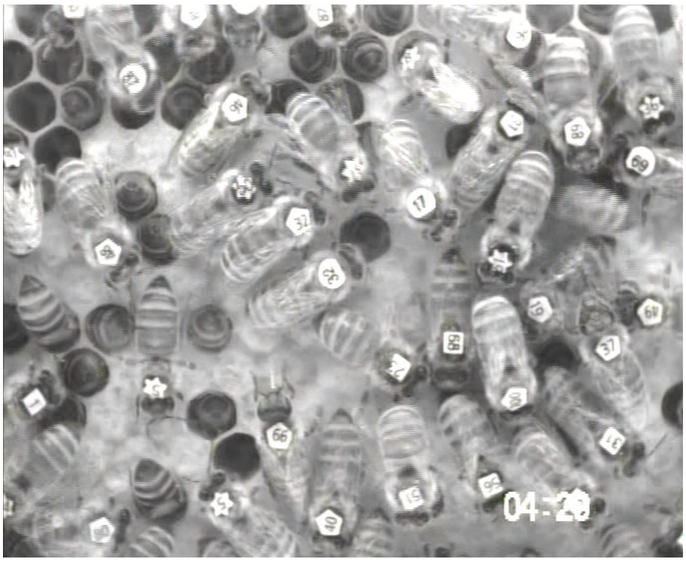


Fig. 2. Typical image of the comb. In our approach bees are treated as clutter which makes an early detection of uncapping difficult.

The preprocessing step results in sets of images which show the surface of the brood cell. Each set contains images of just a single brood cell. As an option the images can be transformed to have an equal mean gray value. This kind of normalization improves the evaluation of the image sets by a human expert because it helps to focus on more relevant changes of the surface.

SEGMENTATION OF IMAGES

Ideally, at this point of processing the image sets only consist of images without bees, but typically, a couple of such images passes the mentioned prescreening step. Therefore, extraction and evaluation of potential openings must be performed. We decided to rely on two features of the small defects on the cap of a cell:

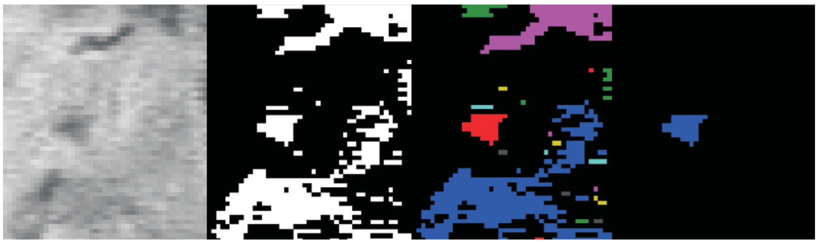
- dark and compact appearance compared to their neighborhoods and
- their fixed positions.

We assume, that the first feature allows the segmentation into foreground (the opening) and background regions (the rest). The second feature allows to exclude isolated bee eyes or extremities which are typical sources of error. A contrast-limited adaptive histogram equalization is applied to improve the first feature.

In [5], Balthasar et al. proposed an efficient technique for analyzing of 1D histograms. Originally used for the extraction of typical color values, this technique can also be applied for the required adaptive segmentation of images. The method is based upon the search for peak values (local maxima) in the distribution. Additionally, the label of the nearest peak value is assigned to each histogram bin. This method can be used for an adaptive binarization of cell images as follows:

- FIND the number n of local maxima M_i of the gray value histogram
- DIVIDE the histogram into segments S_i, one for each maximum M_i
- SORT list of segments by M_i
- INITIALIZE a binary image B of same size as the original image (all pixels $B_{x,y}$ are set to zero)
- FOR EACH segment
    - GENERATE a binary image mask K for all pixels of the original image that have a gray value which belongs to the segment
    - IF the number of non zero pixels in K is lower than a threshold T
        - Update B, such that $B_{x,y} = \begin{cases} K_{x,y}, \text{if } K_{x,y} = 1 \\ B_{x,y}, \text{if } K_{x,y} = 0 \end{cases}$
    - ELSE
        - BREAK (skip all remaining segments)

This procedure excludes all homogenous regions larger than a certain threshold *T*. Fig. 3 shows the segmentation results for a single image.



A B C D

Fig. 3. (A) original image, (B) foreground image, (C) labeled connected components, (D) classified as opening

Binarization of the images in terms of background-foreground estimation can also be based on models of the appearance of the brood cells. So called *intrinsic images* [6,7] seems to be an adequate and robust method. Other techniques like Gaussian mixture models can also be applied [8]. A disadvantage of these approaches is the need for a sufficient large number of images to create a reliable model.

A sequence of masks can be combined to increase the confidence, because an opening persists for a certain time until the brood cell is closed again or has been fully uncapped. Hence we recursively calculate an average image $\overline{B}$. The parameter α controls the update rate.

$$\overline{B}_t = (1-\alpha)\cdot \overline{B}_{t-1} + \alpha \cdot B_t$$

For binarization of the image $\overline{B}$ a fixed threshold is recommended. The threshold value depends on α and the difference $\Delta t = t_i - (t_{i-1})$. Due to the nature of prescreening (which eliminates occlusion, see [4]) Δt is not constant.

Fig. 4 shows the input images, the segmentation results, and the evolution of the average image.

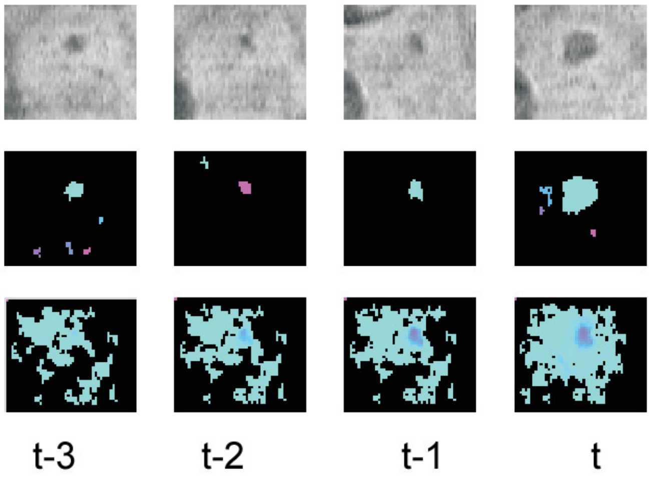


Fig. 4. Sequence of images (top row), extracted regions (middle row), color coded average mask $\overline{B}$ (bottom row)

CANDIDATE SELECTION

An evaluation of the candidate regions is required to reduce or eliminate false alerts. A set of criteria has been checked for 1400 images of openings (taken from 28 cells at different times) and approximately 142,000 images with an intact cell cap.

Among the criteria are:

- Minimum distance from image boundary
- Size of region
- Different measures for the compactness of a region
- The ratio between the update rate α and the threshold for binarization of $\overline{B}$

If an image contains a connected component which meets the criteria, the detection of an opening is reported. We minimized a cost function in order to find suitable parameters for all criteria. The cost function was defined as the weighted number of misclassifications. A false negative classification was penalized with a cost factor of 10,000 to compensate the higher number of negative examples and to emphasize the need to detect the openings as early as possible. A false positive classification is penalized with a cost of only 1. By varying the parameters systematically within reasonable intervals we obtained a set of optimal parameters for the defined cost functions.

With this approach 61 % of the openings are reported. If we count the reported brood cells then the detection rate increases to 79 %. Reducing the cost of a false negative classification results in a more sensitive classifier. On the other hand, this would lead to a further loss of specifity.

CONCLUSIONS

We have presented a robust method for the segmentation of openings of honeybee brood cells. The segmentation can be improved by averaging.

The described approach for the automatic detection of (small) openings marks still a beginning. The sensitivity of the detector is already acceptable to improve the process for genetic selection of bees. However, the number of false alerts exceeds the true ones by factor 36. Hence future work must concentrate on more specific classifiers. Despite this limitation current experiments at the *Länderinstitut für Bienenkunde Hohen-Neuendorf* already benefit from the detector. The presented method complements the generation and analysis of reports by further reducing the number of irrelevant images.

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