Algorithm for Detection of Single Isolated Human Insulin Crystals for In-Situ Microscopy

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CERMA 2012, Cuernavaca, Morelos, Mexico, November 2012

Overview

- Introduction
- Problem
- Approach
- Algorithm
- Experimental results
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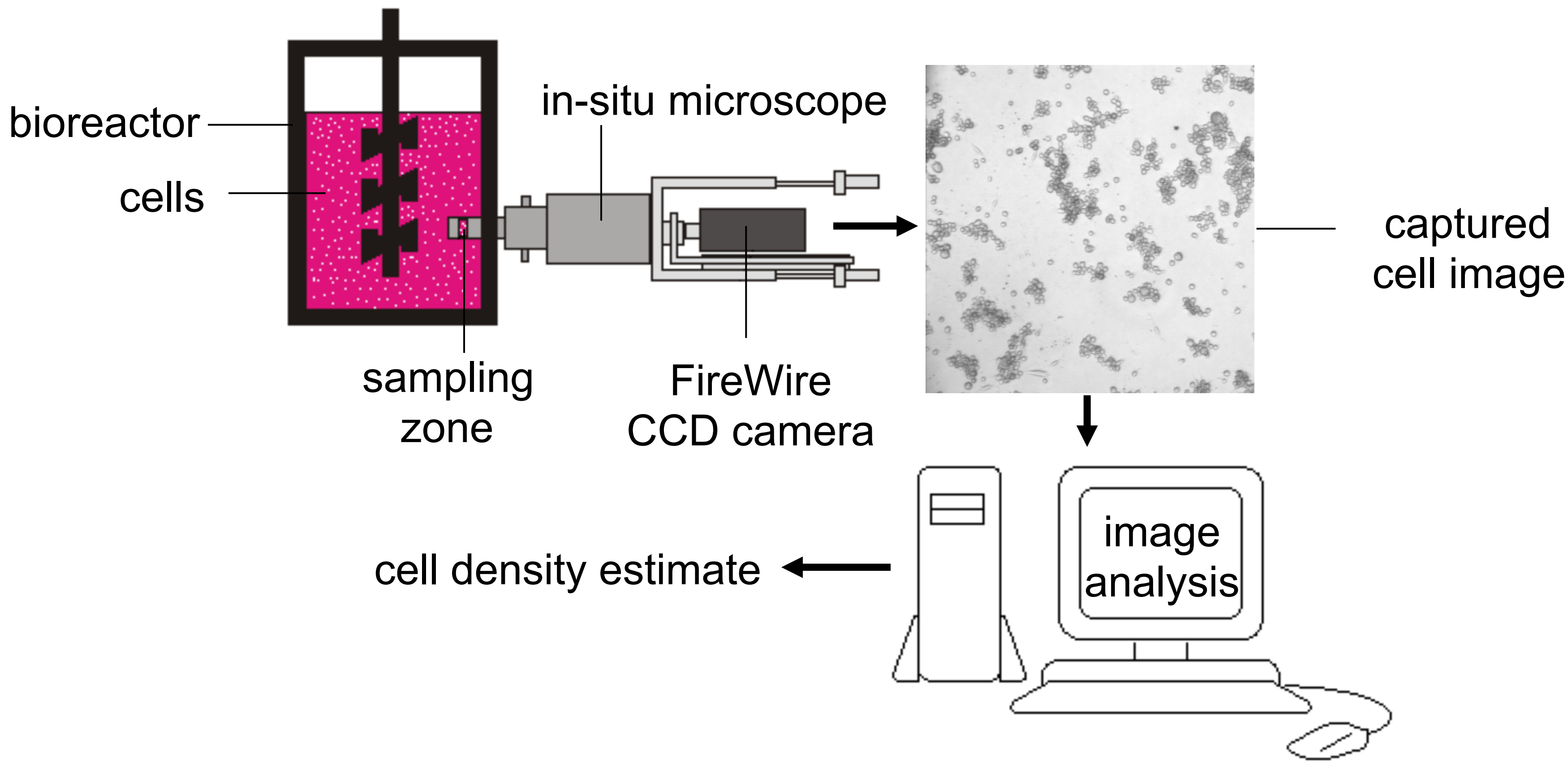
Introduction

On-line automatic cell density estimation with no risk of culture contamination

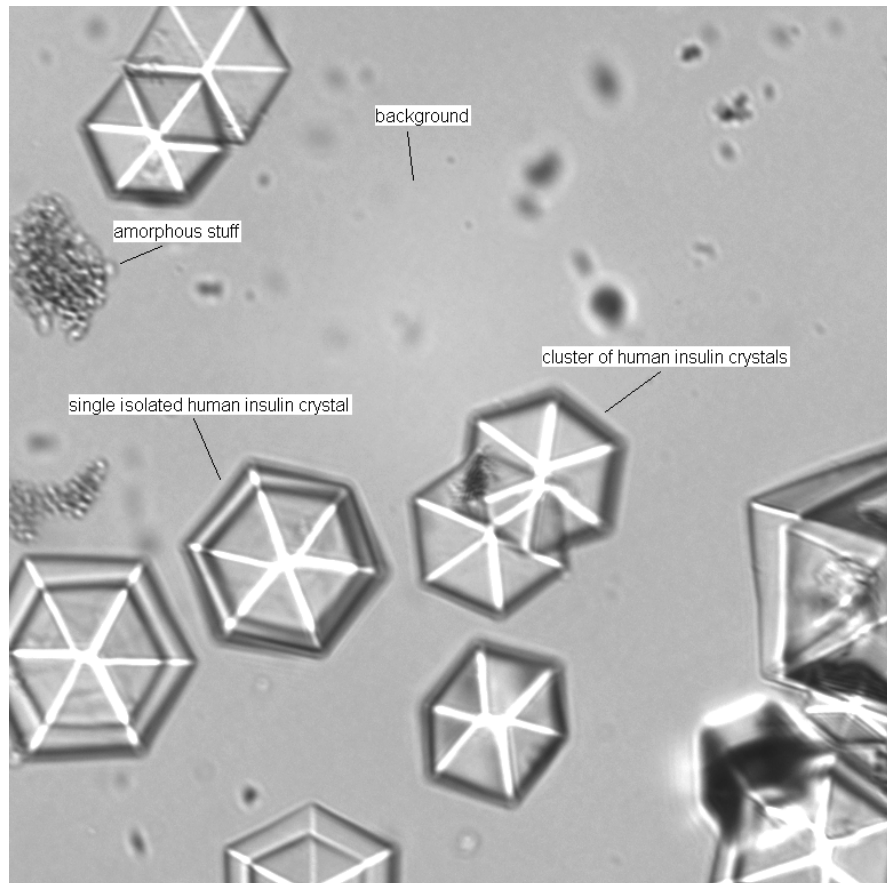


Introduction

As an alternative, we are using the in-situ microscope for on-line analysis of human insulin crystallization processes

Images of first experiments show:

- Homogeneous background
- 4 different classes of foreground regions C_n, n=0,…3: single crystals (C_0), crystal clusters (C_1), amorphous stuff (C_2) and mixed regions (C_3)

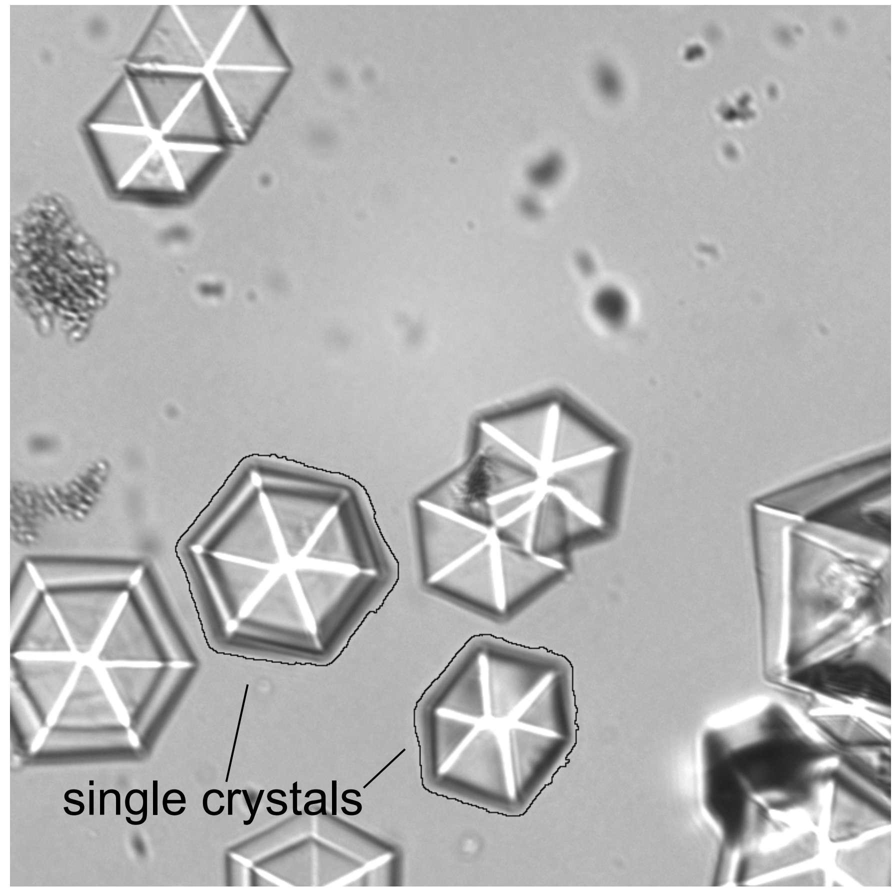


Human insulin crystal image captured by an in-situ microscope

Problem

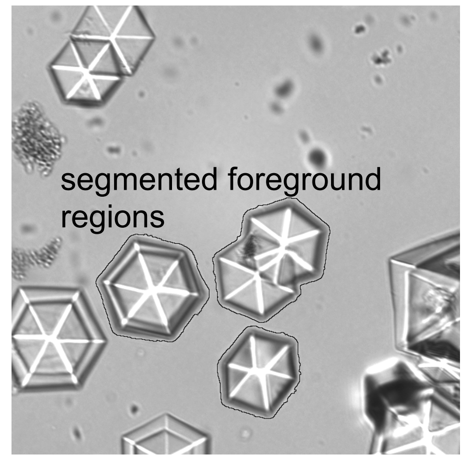
We are interested in the regions of the single crystals!

but how can them be automatically found in the captured images?

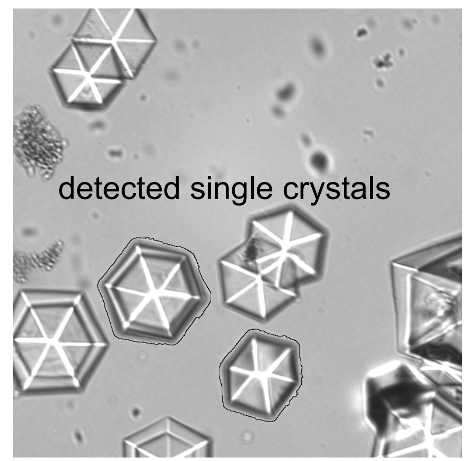


Two-Staged Approach

- First, all the foreground regions are segmented



- Then, the single crystals are detected among the segmented foreground regions



Two-Staged Approach

Foreground Region Segmentation

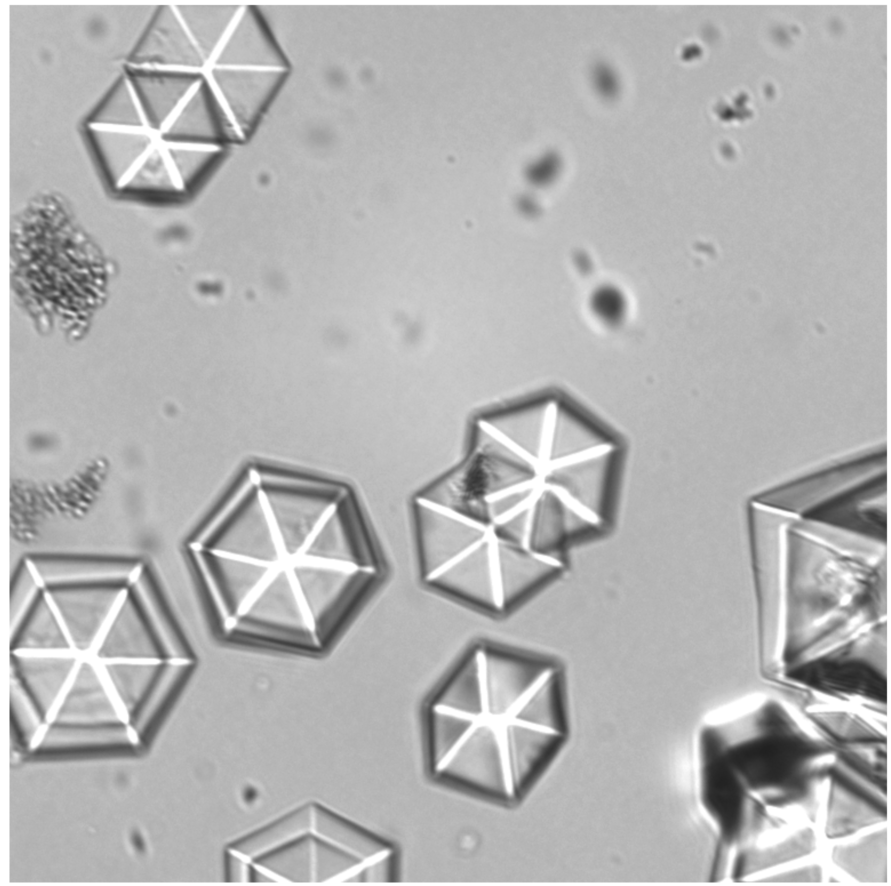
- Pixel classification based on the evaluation of the local intensity variance:
  - pixels whose local intensity variance is less than a threshold th_g are classified as belonging to the background regions, otherwise they are classified as belonging to the foreground regions

Single Crystal Detection

- Single nearest shape prototype detection:
  - a foreground region is detected as a single crystal if in the Euclidian space its shape is much closer to the shape prototype of the single crystals than to the shape prototypes of the other classes of foreground regions

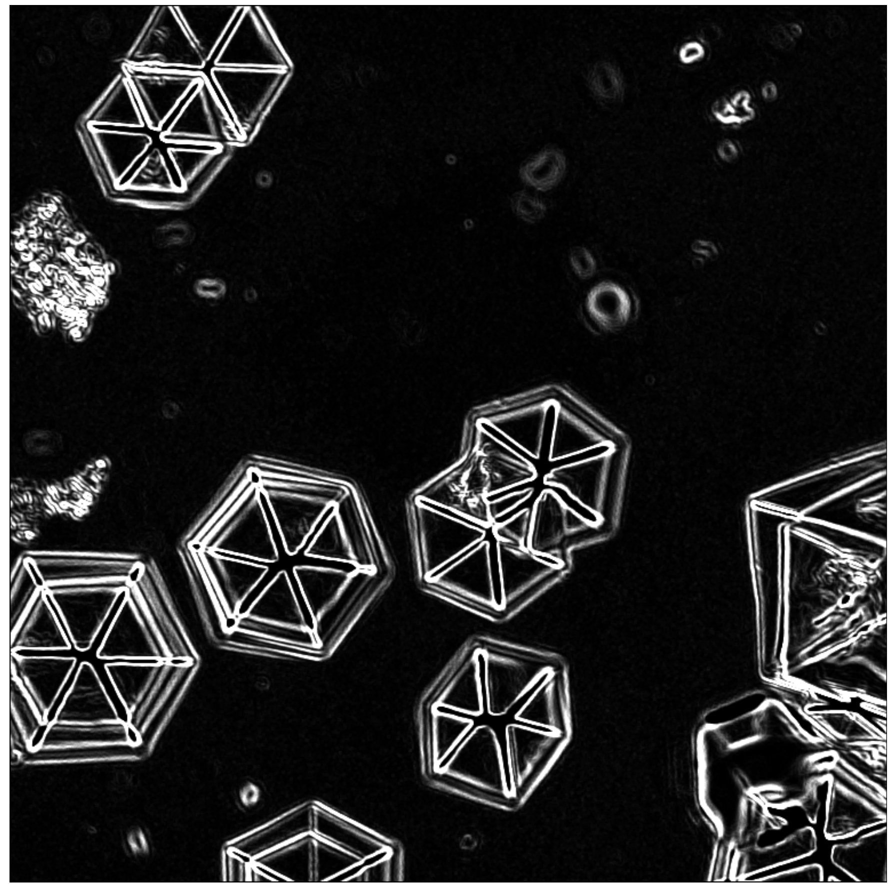
Algorithm

1) Capture an intensity image I



Algorithm

2) Estimate the local intensity variance at each pixel position



Algorithm

3) Classify all the pixels of the variance image V into pixels belonging to the foreground regions and pixels belonging to the background region by using the global threshold th_g

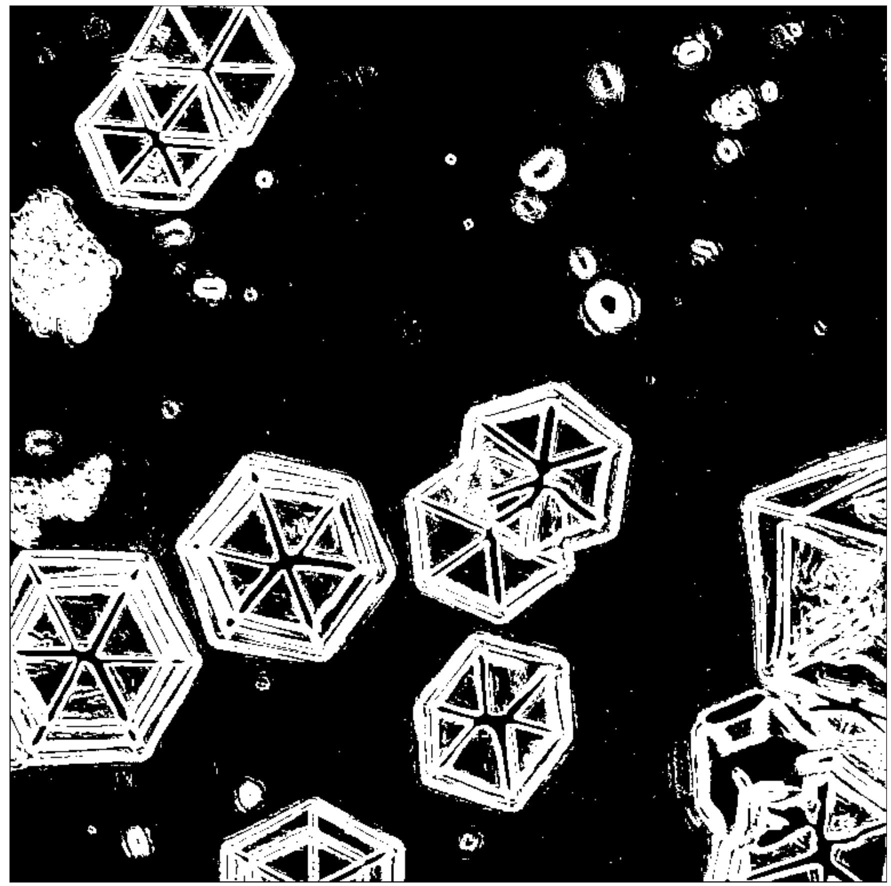
   $V_i \leq th_g$: background (black)

   $V_i > th_g$: foreground (white)

   where $th_g = m_1 + 4\sigma_1$

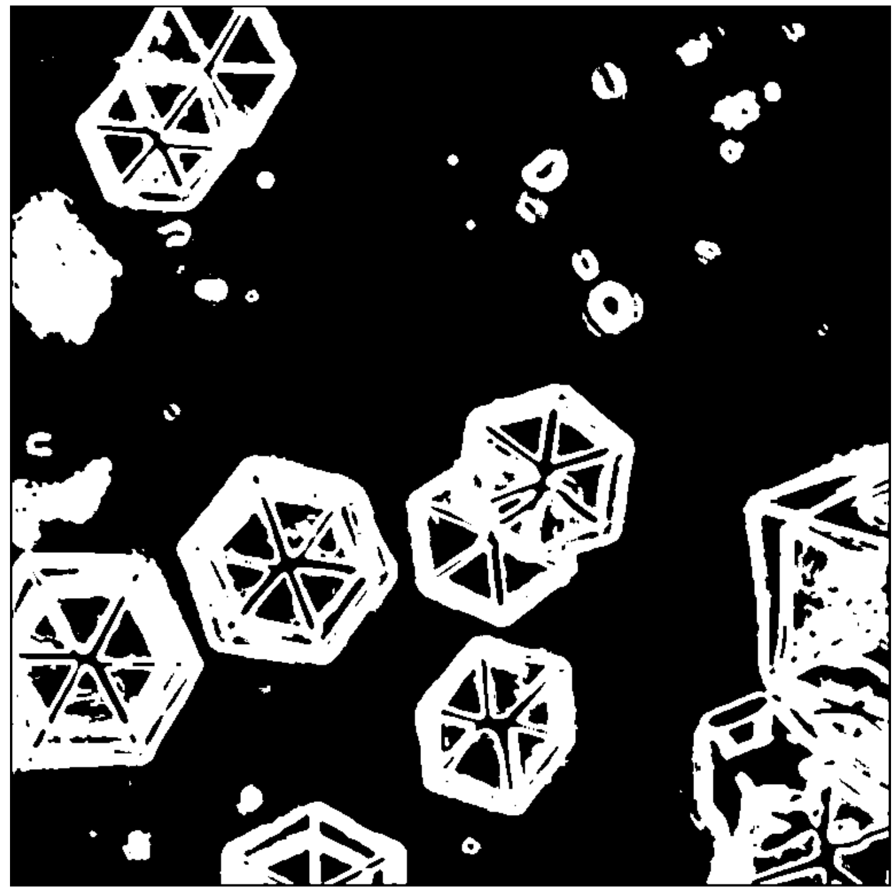
   σ_1: standard deviation of the variance values at the background

   m_1: mean of the variance values at the background



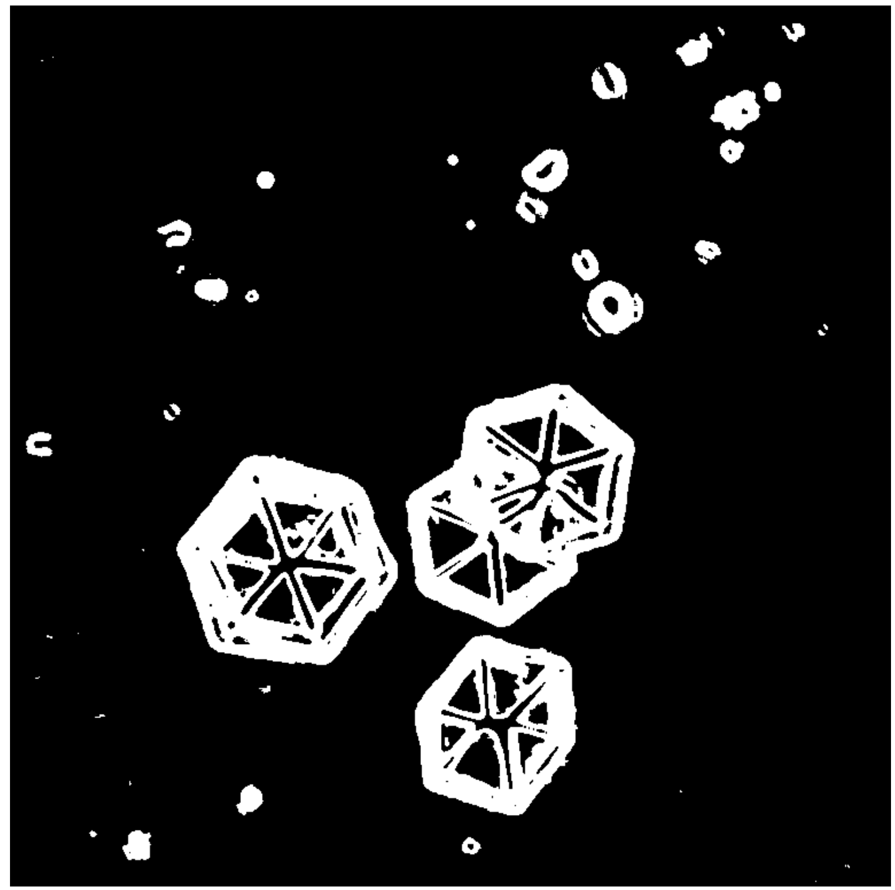
Algorithm

4) Eliminate isolated white pixels by applying a 5x5 median filter



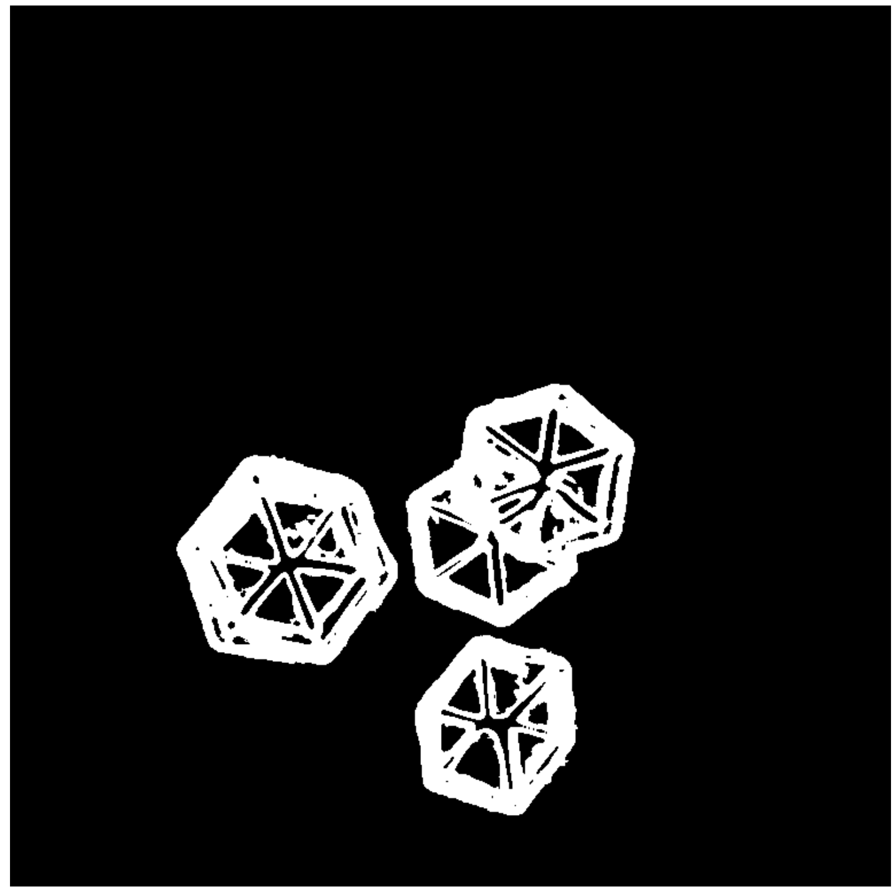
Algorithm

5) Eliminate any white region touching any image border



Algorithm

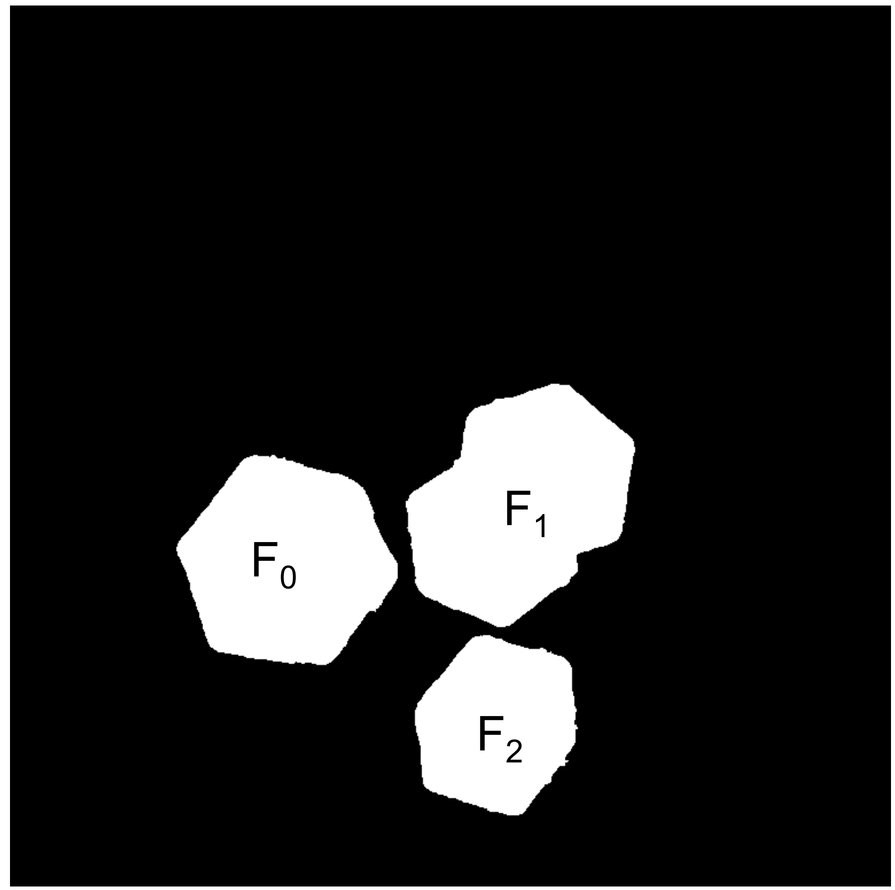
6) Eliminate white regions whose image area is less than 0.09% of the total image area



Algorithm

7) Eliminate black holes inside white regions

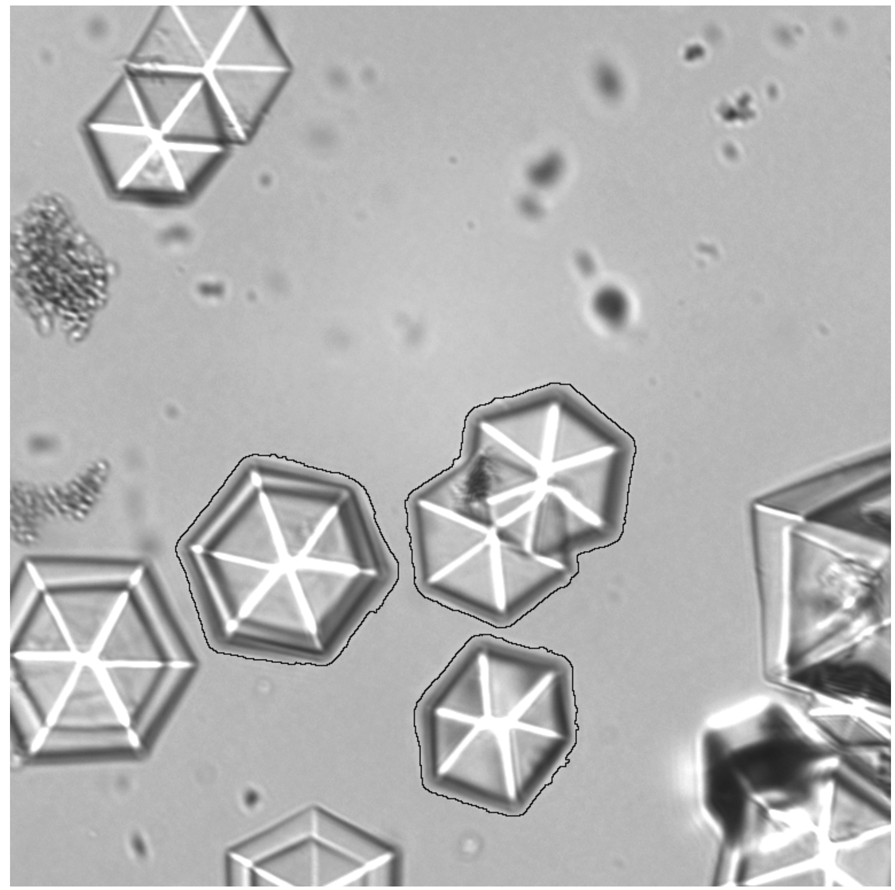
   The remaining white regions represent the segmented foreground regions F_s, s=0, …,S-1



F_s, s=0, 1, 2

Algorithm

8) Compute for each segmented foreground region F_s a 7-dimensional vector of rotation, translation and scale invariant shape characteristics $C_s(k)$, k=0, …, 6, according to M.-K. Hu



Algorithm

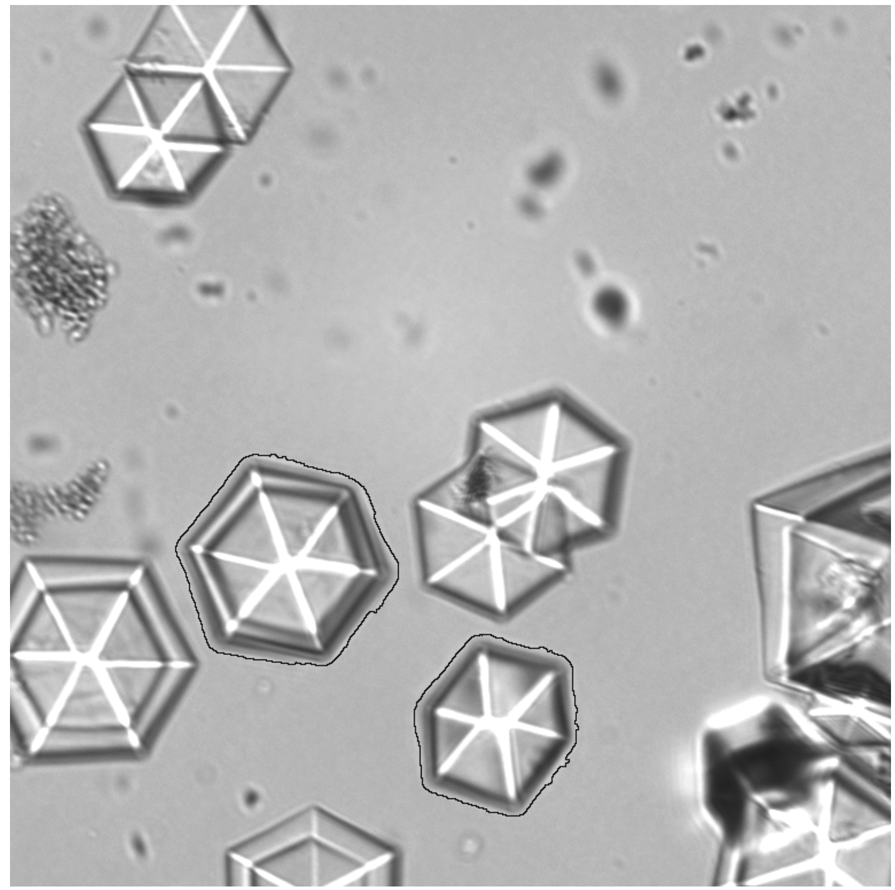
9) Detect an arbitrary segmented foreground region F_s as the region of a single crystal if its shape vector C_s is much closer to the shape vector prototype P_0 of the single crystals than to the shape vector prototypes P_1, P_2 and P_3 of the other classes of foreground regions

$$\left\| C_s - P_0 \right\| \leq \left\| C_s - P_n \right\|, \forall \; n = 0,..,3$$

where

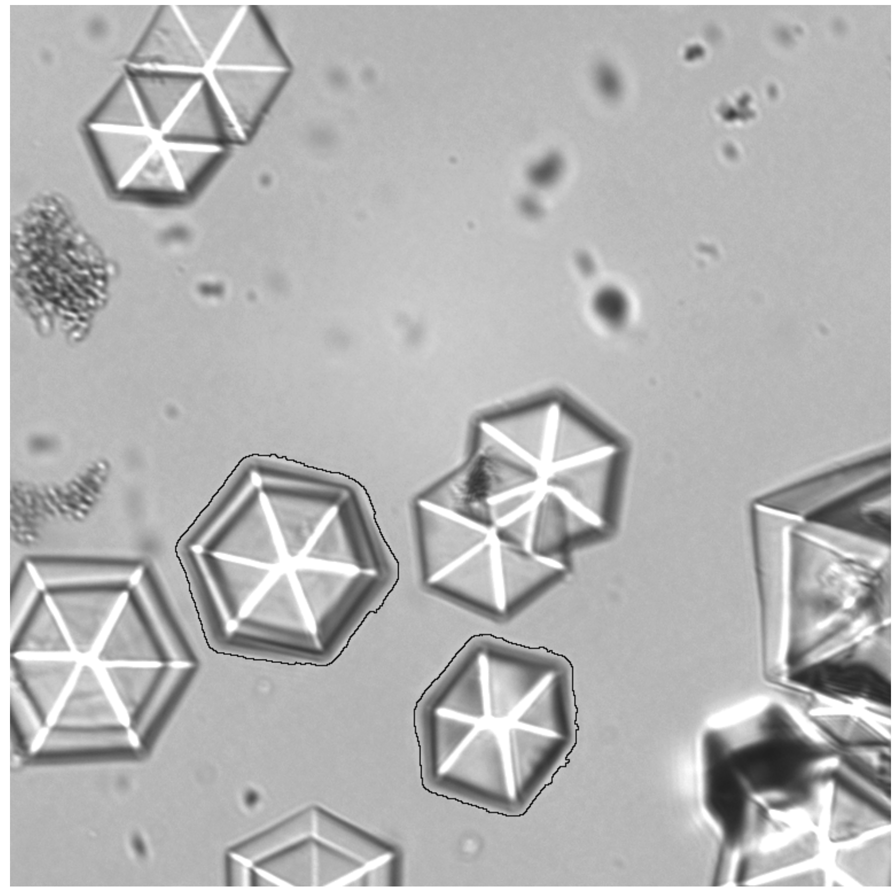
$$\left\| C_s - P_n \right\| = \sqrt{\sum_{k=0}^{6} \left(P_n(k) - C_s(k) \right)^2}$$

The shape vector prototypes are computed a priori from a training set of images

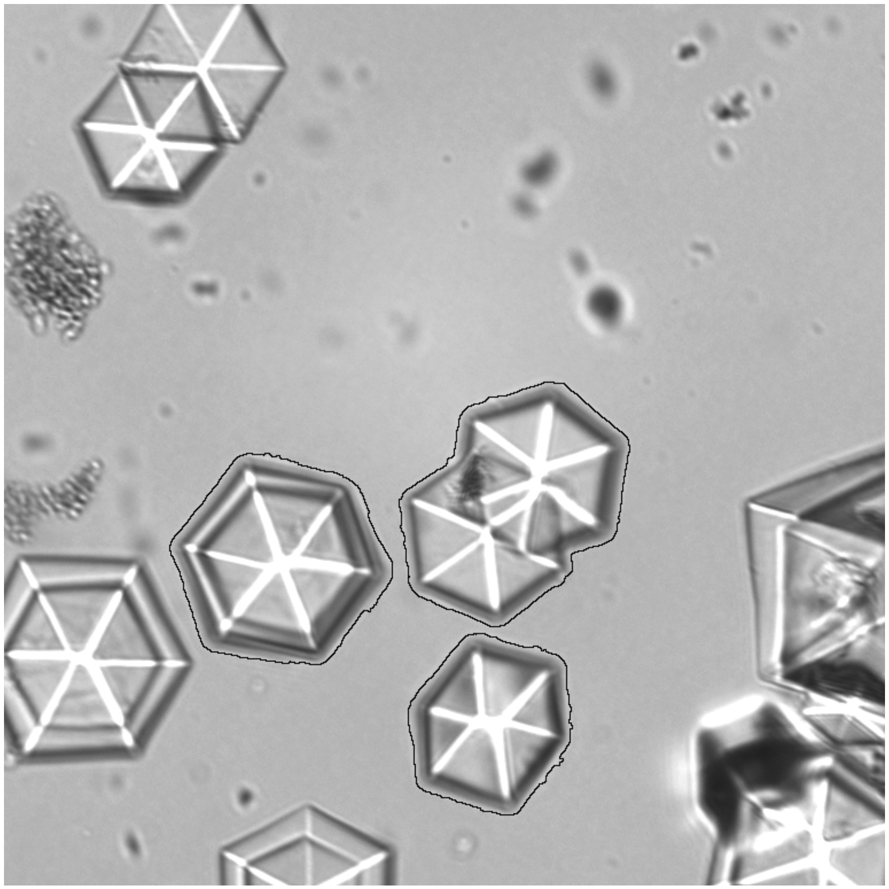


Experimental Results

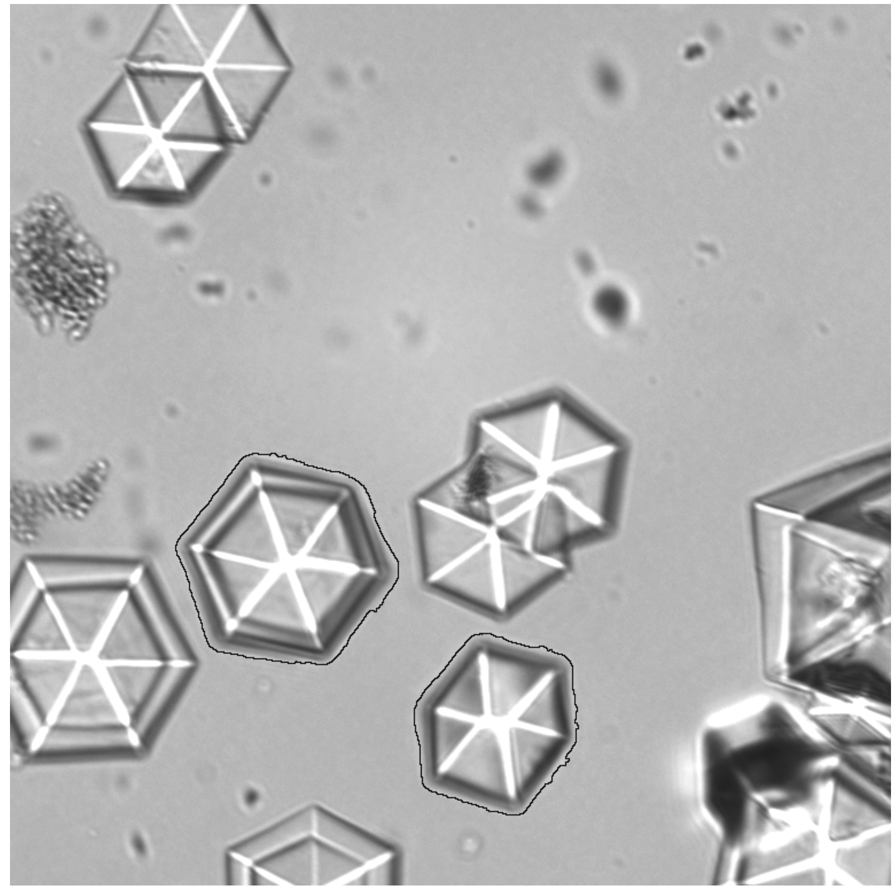
- Implemented in C under Windows XP
- Intel Core Duo CPU at 2.2 GHz and 2 GB RAM
- Tested with 289 real images
- Average processing time of 0.15 sec/image
- Detection reliability (F score) of 95%



Experimental Results

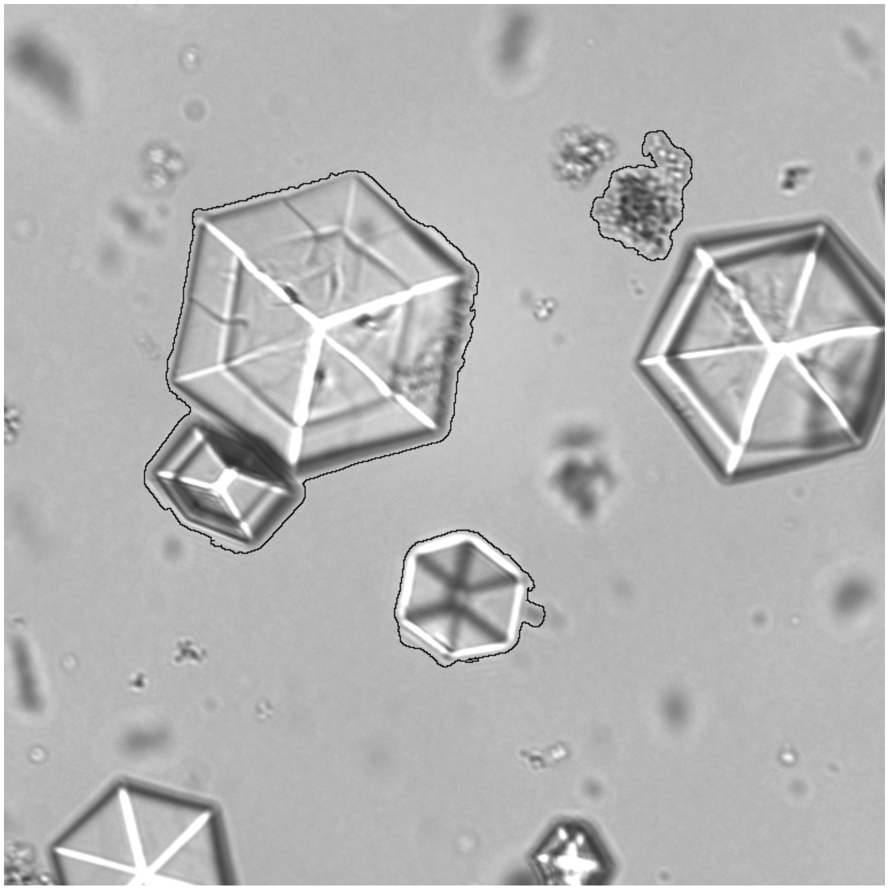


Segmented foreground regions

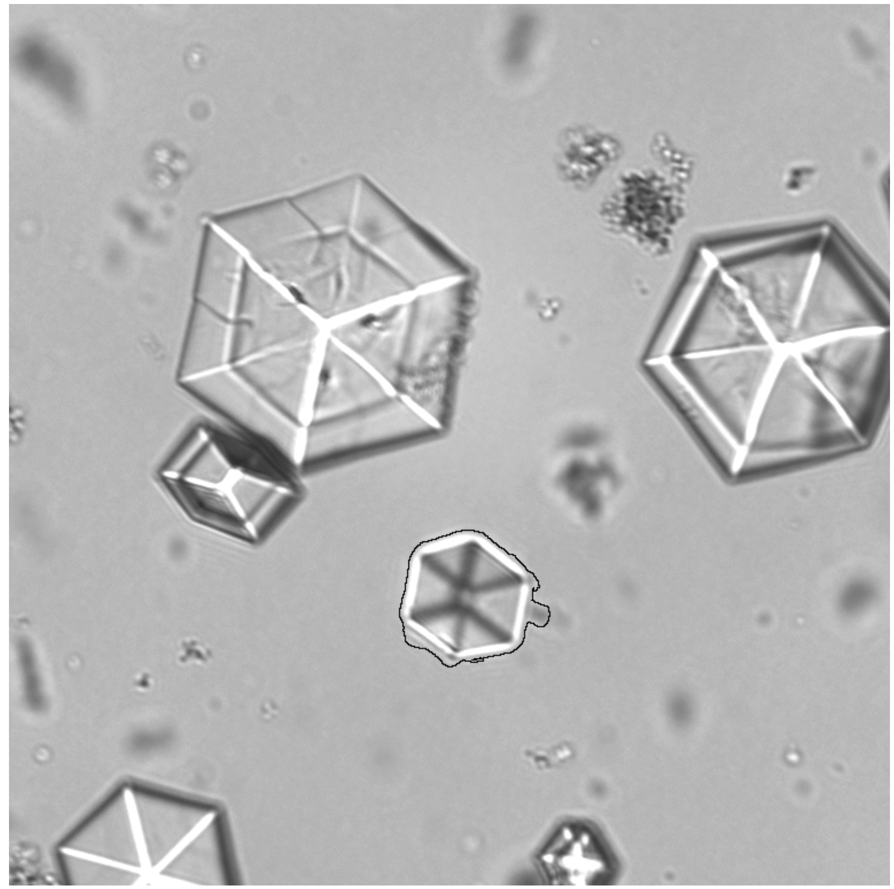


Detected single crystal regions

Experimental Results



Segmented foreground regions



Detected single crystal regions

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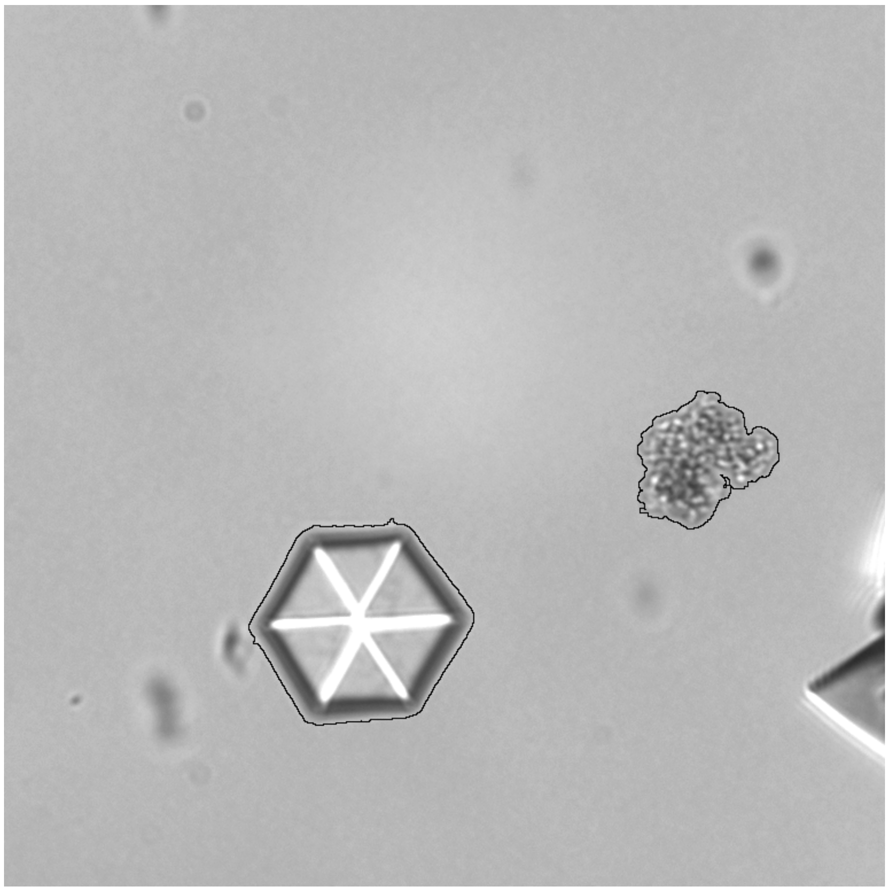
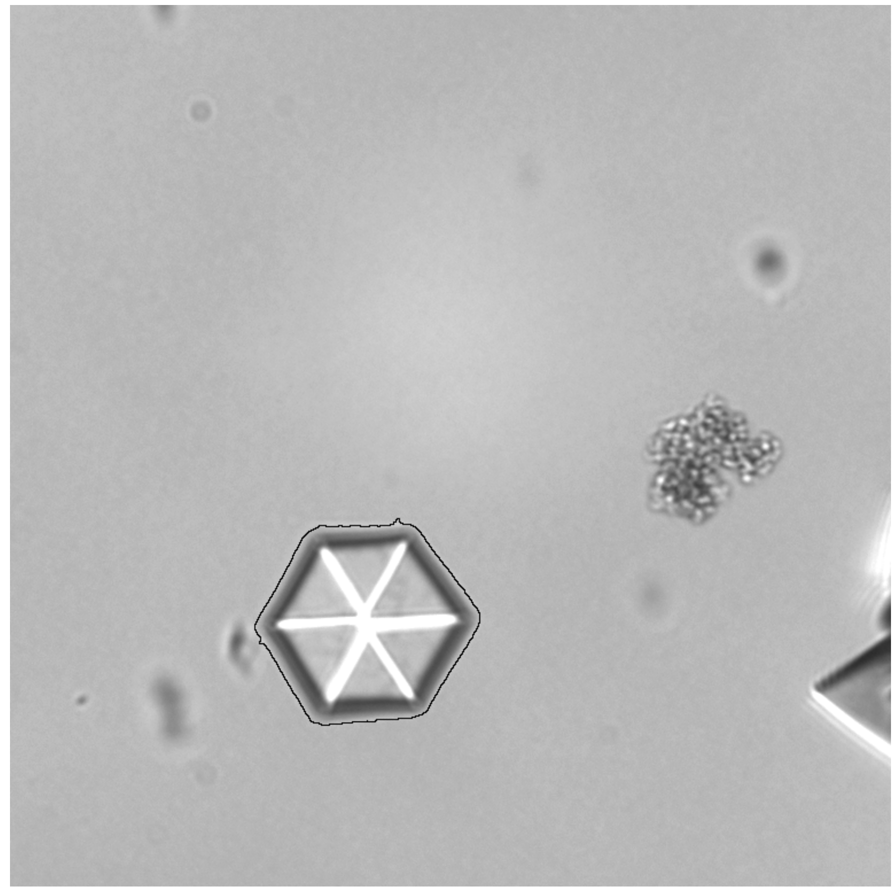
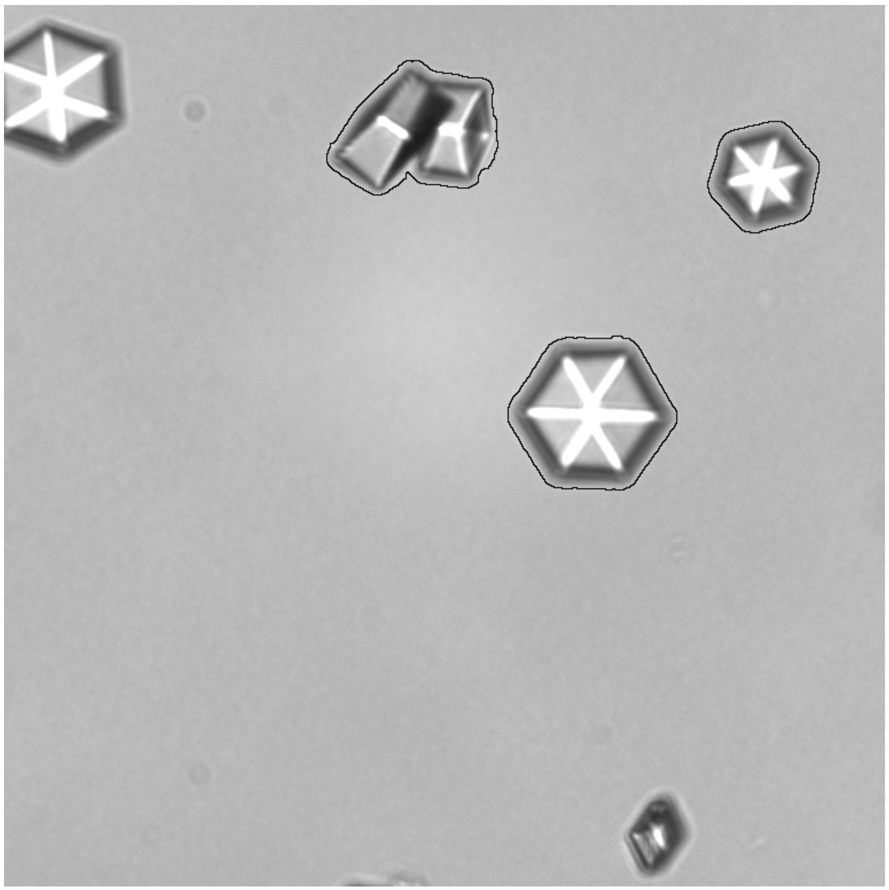


Segmented foreground regions

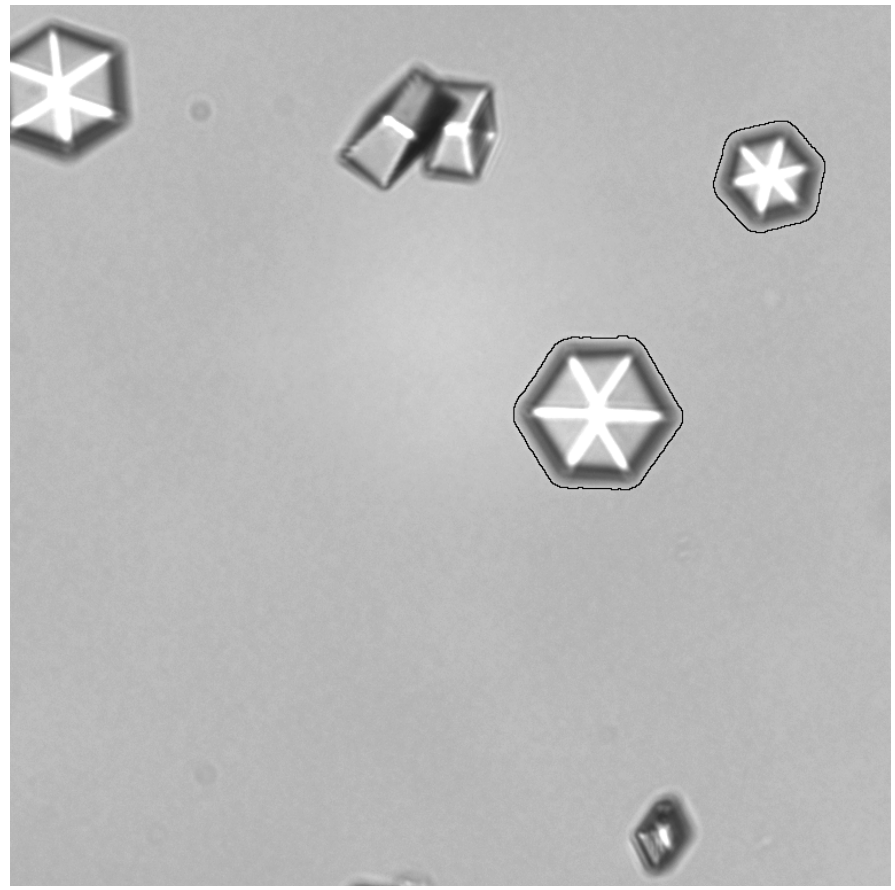


Detected single crystal regions

Experimental Results

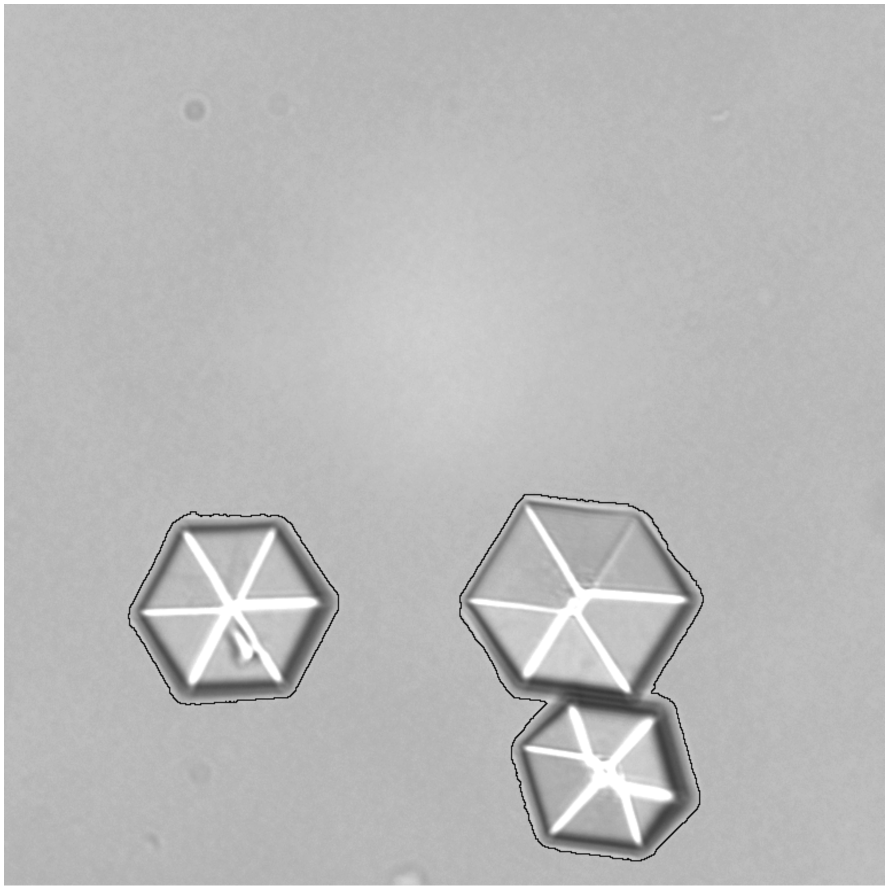


Segmented foreground regions

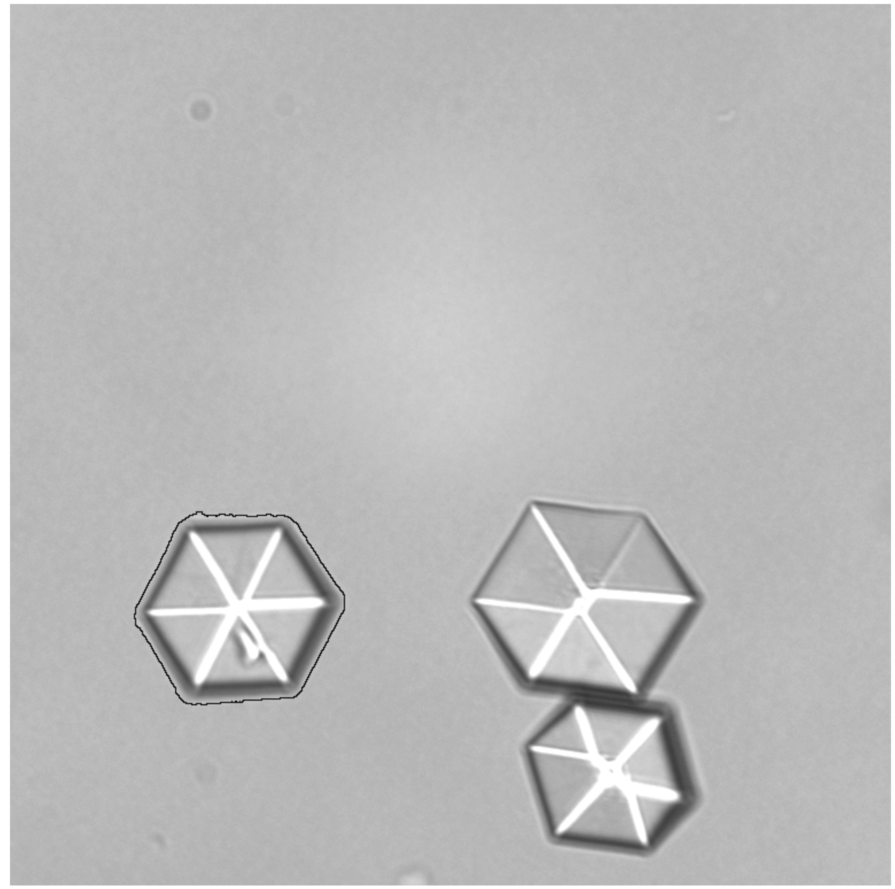


Detected single crystal regions

Experimental Results

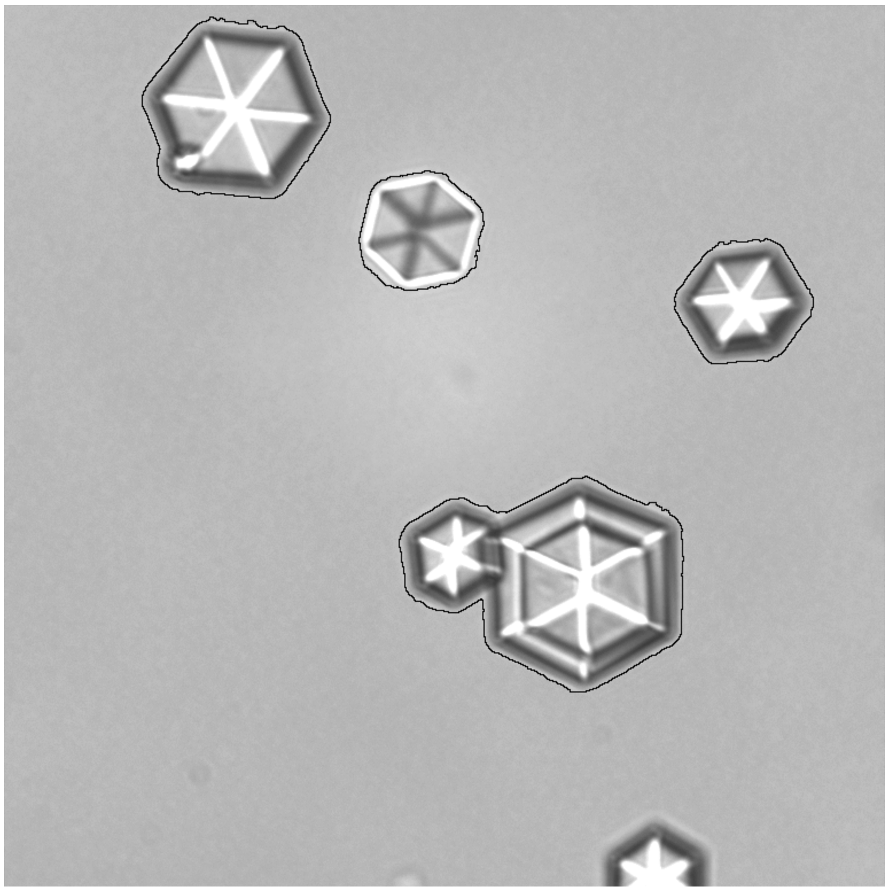


Segmented foreground regions

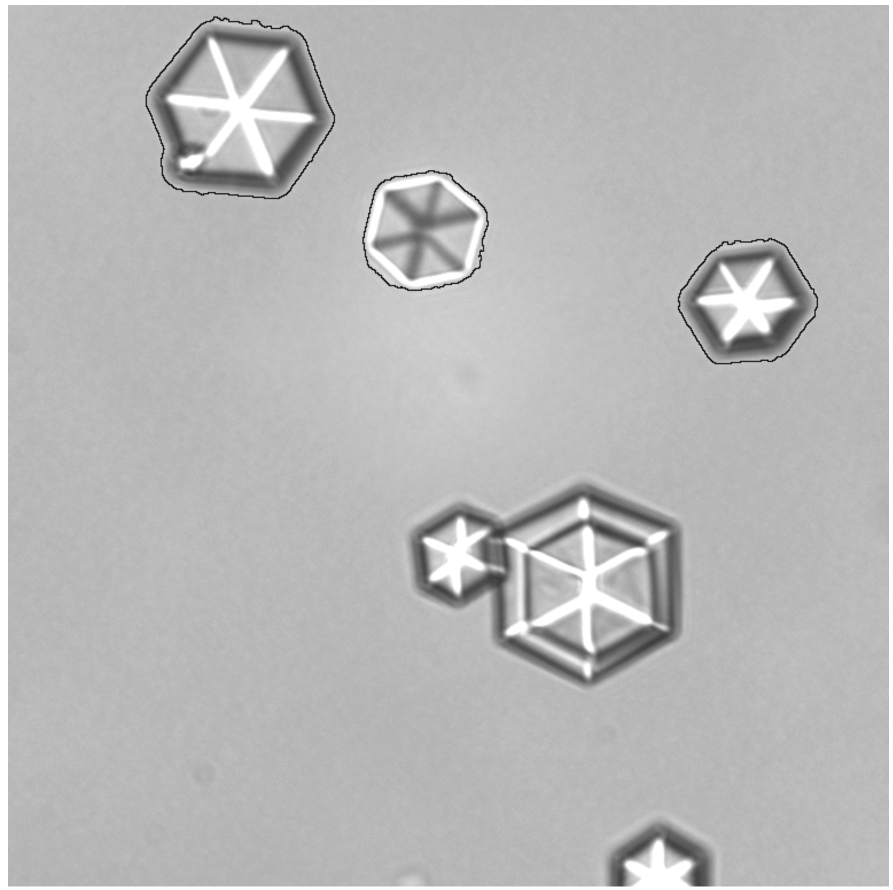


Detected single crystal regions

Experimental Results



Segmented foreground regions



Detected single crystal regions

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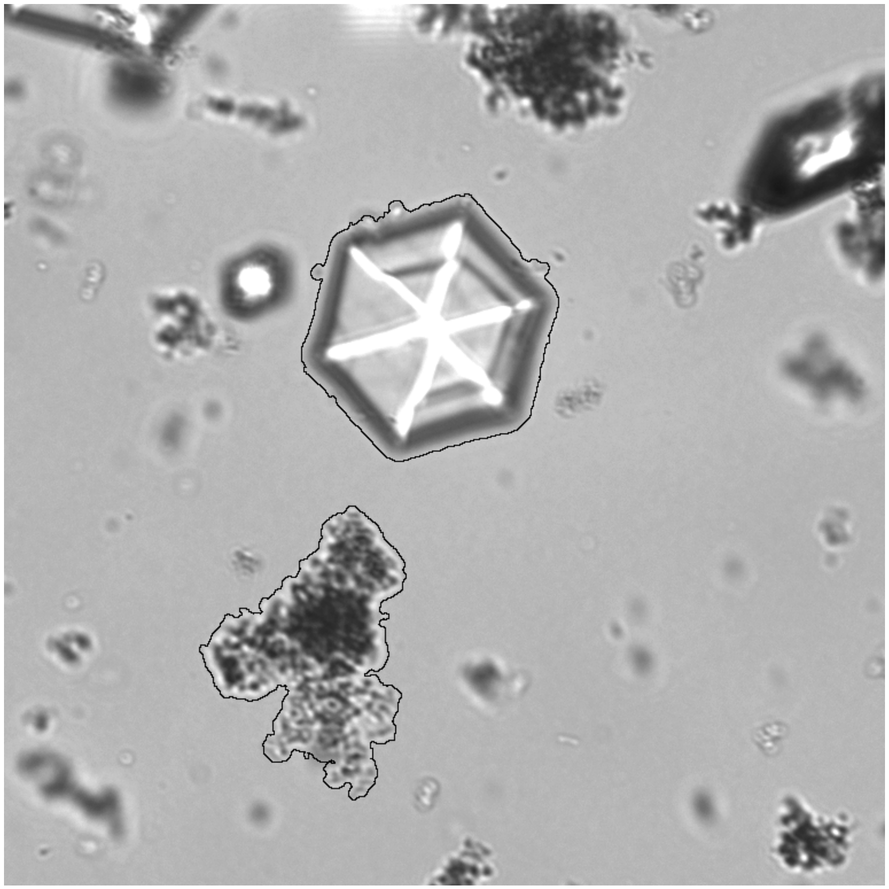
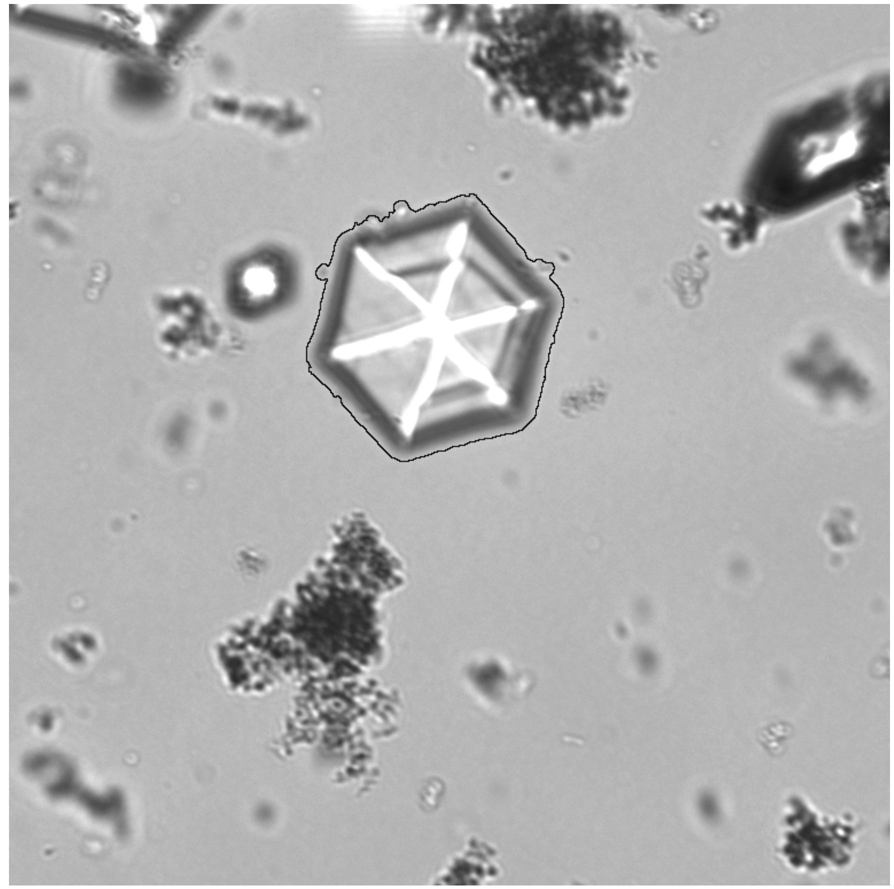
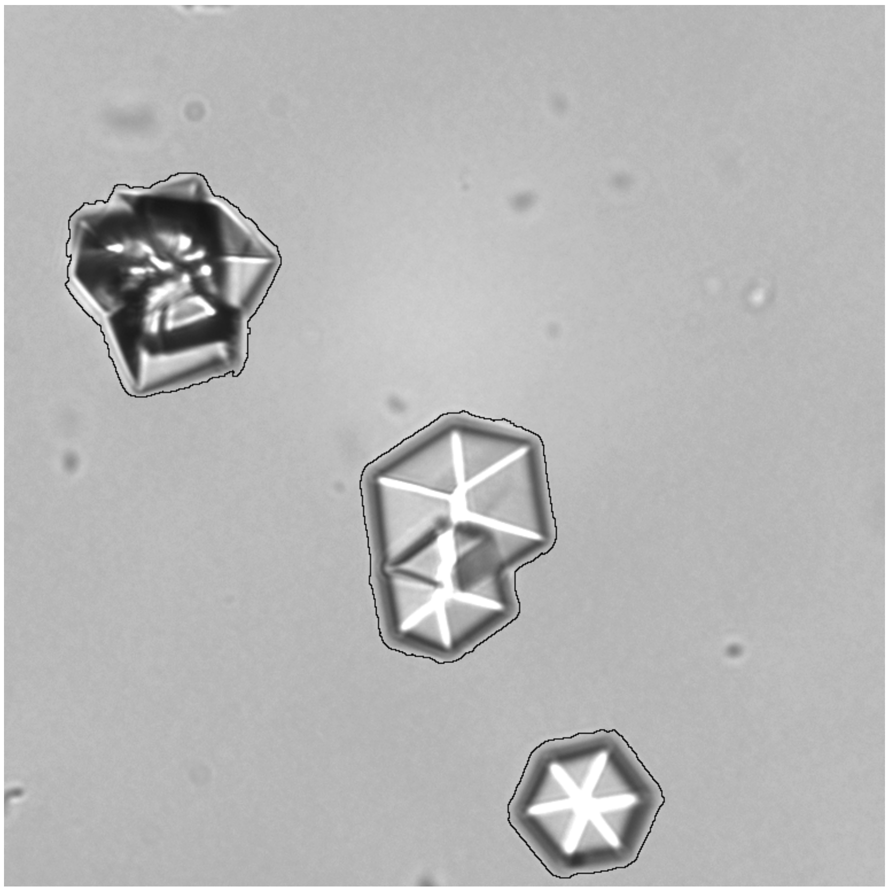


Segmented foreground regions

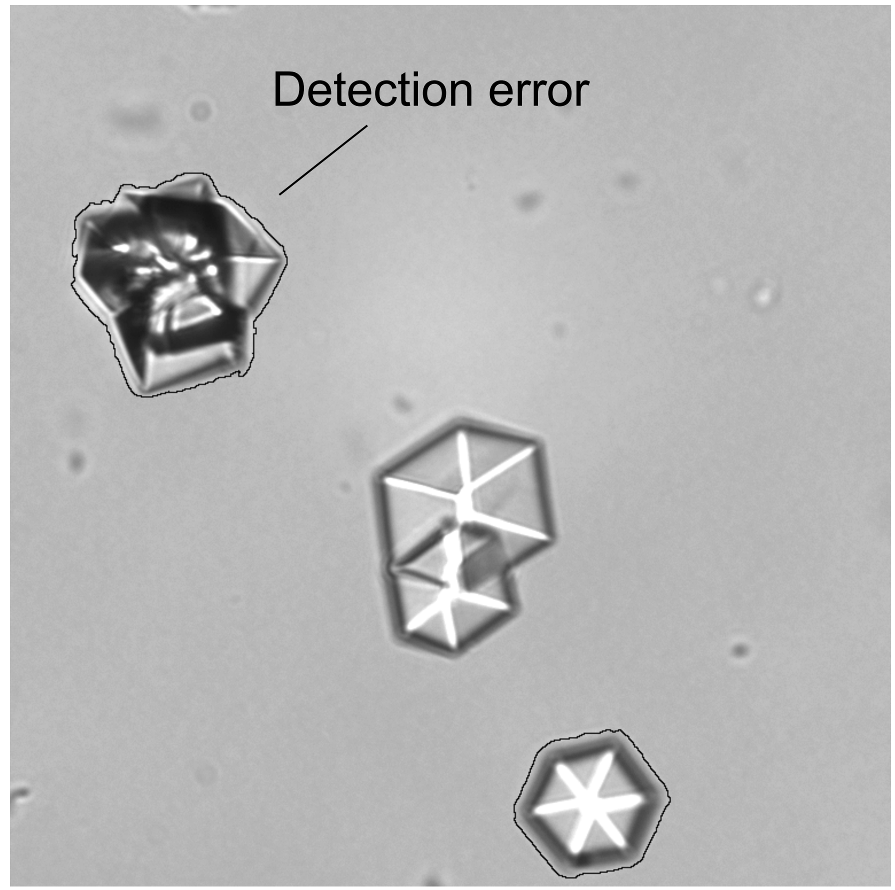


Detected single crystal regions

Experimental Results



Segmented foreground regions



Detected single crystal regions

Summary

- First, the foreground regions are segmented by using a global threshold technique. Then, an arbitrary segmented foreground region is detected as the region of a single crystal if in the Euclidian space its shape vector is much closer to the shape vector prototype of the class of regions of single crystals
- A shape vector is a 7-dimensional vector of rotation, translation and scale invariant shape characteristics
- The Euclidian distance is used to compute the closeness between shape vectors
- Tested with 289 real images captured by the in-situ microscope
- Average processing time of 0.15 sec/image
- Detection reliability of 95%

Contact Information

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