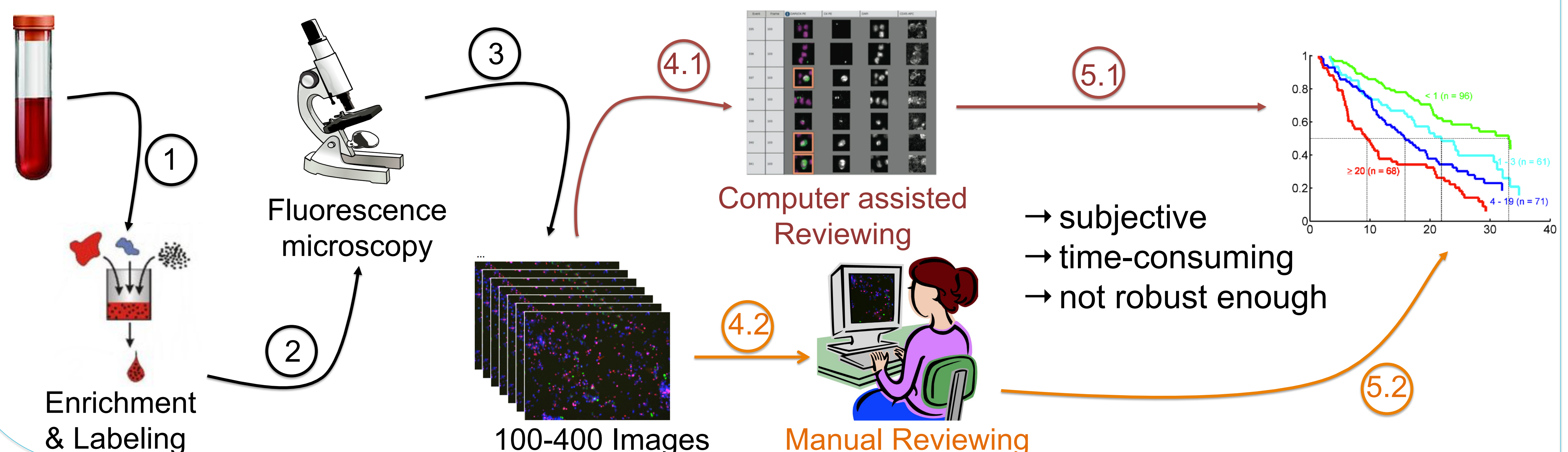# Identifying Circulating Tumor Cells (CTCs) by Image Analysis

Leonie Zeune[1,2], Christoph Brune[1], Stephan van Gils[1], Guus van Dalum[2], Leon Terstappen[2]

[1]Applied Analysis and [2]Medical Cell Biophysics Group, MIRA, University of Twente

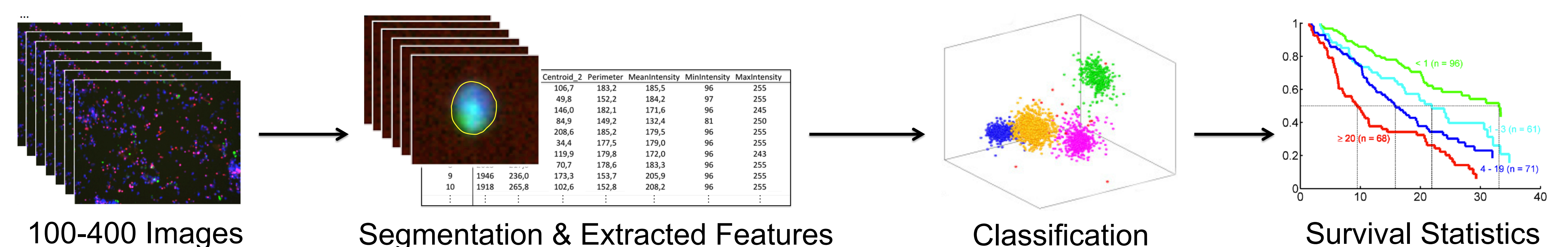**MIRA** — BIOMEDICAL TECHNOLOGY AND TECHNICAL MEDICINE

Introduction

The Cancer-ID consortium aims to validate blood-based biomarkers for cancer.

- cells dissociate from primary tumor and invade blood circulation
- rare cell events, challenging to detect
- CTC count has prognostic value for survival outcome
- no overall CTC definition exists yet

1 → Enrichment & Labeling
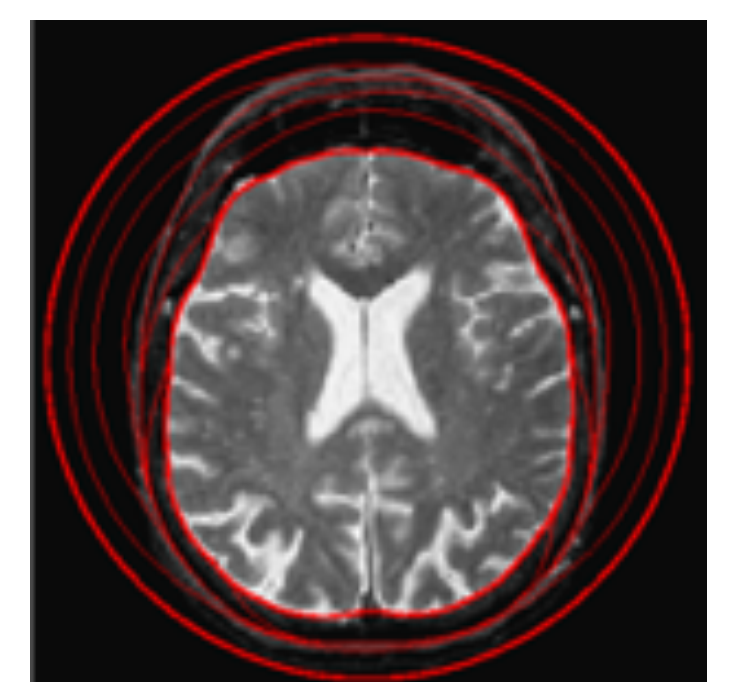2 → Fluorescence microscopy
3 → 100-400 Images
4.1 → Computer assisted Reviewing
4.2 → Manual Reviewing
5.1 → Survival statistics
5.2 →

→ subjective
→ time-consuming
→ not robust enough

Automatic Data Processing

Development of an automated, platform-independent identification algorithm.

100-400 Images → Segmentation & Extracted Features → Classification → Survival Statistics

- sensitivities in data: noise, contrast, background artifacts…
- reliable and efficient segmentation forms basis for further processing

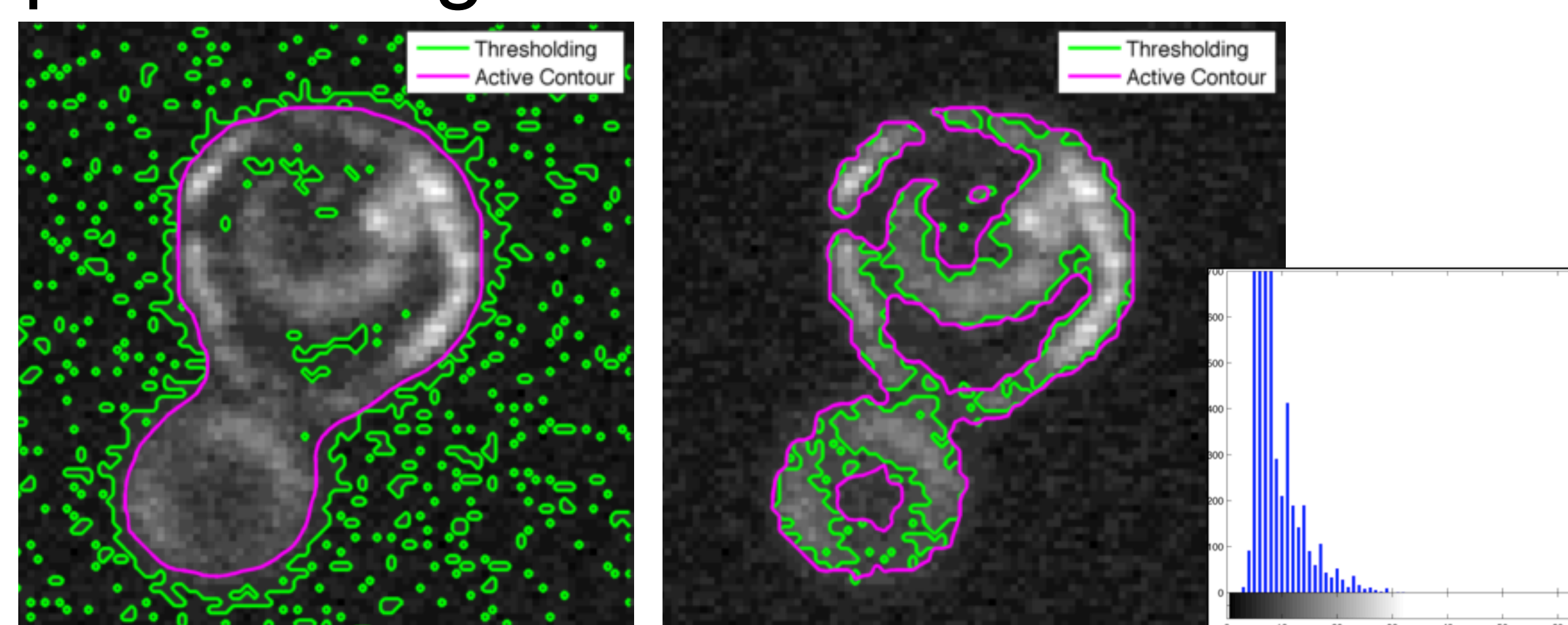Active-contour segmentation energy:

$$J(c_1, c_2, C) = \underbrace{\int_{\Omega_{\text{in}}} |f(x) - c_1|^2 \mathrm{d}x + \int_{\Omega_{\text{out}}} |f(x) - c_2|^2 \mathrm{d}x}_{\text{data discrepancy term}} + \alpha \cdot \underbrace{\text{Length}(C)}_{\text{regularization term}}$$

Results

Improved Segmentation:

increased threshold & decreased α

- improved robustness (esp. against noise)
- α determines segmentation scale

Automated Classification:

- kNN, SVM, PCA

Conclusion / Outlook

- Validation
  - Segmentation: manually segmented cells from MCBP members
  - Classification: manually scored images from CANCER-ID partners
- Robustness
  - improve background artifacts robustness
- Automatic Parameter Choice
  - relation to scale space approaches?
- Advanced Classification Methods

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CANCER ID