## Characterization of Human Sperm Components for an Accurate Morphological Analysis

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#### Introduction



Infertility is a clinical problem more common than is believed that affects up to 15% of couples, with emotional and physiological implications.

#### Introduction

A semen analysis according to standard criteria, is one of the first steps in the evaluation of male partner of an infertile couple.



Rigorous application of existing guidelines + high laboratory standards + emphasis on identifying categories of abnormal sperm heads -> significant clinical utility when deciding for an infertility treatment.

#### Our Problem

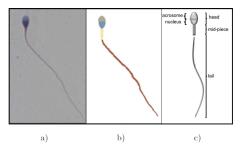


Figure 1: Morphology of the normal human sperm. (a) Representative bright field image of a normal human sperm (Image size:  $277 \times 144$  pixels  $\approx 58 \times 31$   $\mu$ m). (b) Manually segmented ground-truth of the sperm: Head, acrosome, nucleus, mid-piece and tail of stained spermatozoa. (c) Schematic drawing of the principal components of a normal human sperm. Oval head:  $5\mu$ m long and  $3\mu$ m wide. Acrosome: 40 - 70% of the head area. Mid-piece:  $5\mu$ m. Tail:  $55\mu$ m.

#### Our Problem

The computer assisted sperm morphology assessment has been fueled by:

- Inherent lack of objectivity in the evaluation of human sperm morphology
- Difficulty in standardizing, implementing and controlling manual methods
- High degree of variation within and between laboratories and technicians

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## Previous Approaches to Morphological Analysis

There are few approaches to evaluate semen samples automatically, even though none of them proposes a complete framework:

- Park et al. (1997): segmentation of sperm heads using the strategic Hough Transform.
- Nafisi et al. (2005): detection of sperm cells (including tail) using best-fit ellipses.
- Carrillo et al. (2007): segmentation of sperm heads and mid-pieces using thresholding and morphological masks.
- Bijar et al. (2012): segmentation of sperm acrosome, nucleus, mid-piece and identification of tails using a Bayesian classifier with entropy based expectation maximization and a Markov random field.



Gold-standard
Framework for Sperm Cell Segmentation
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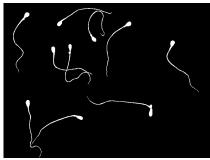
- Built with the cooperation of a referent expert in the field.
- Twenty images with more than two hundred sperm cells plus hand-segmented masks.
- morfologia.cedai.cl/public



#### Gold-standard

Framework for Sperm Cell Segmentation Detection of Sperm Heads Segmentation of Sperm Heads Segmentation of Acrosome and Nucleus Experimental Results





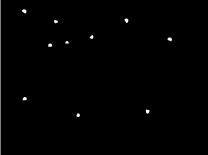
# Gold-standard Framework for Sperm Cell Segmentation Detection of Sperm Heads Segmentation of Sperm Heads Segmentation of Acrosome and Nucleus





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#### Gold-standard

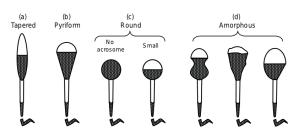
Framework for Sperm Cell Segmentation Detection of Sperm Heads Segmentation of Sperm Heads Segmentation of Acrosome and Nucleus Experimental Results





- 26 normal sperm cells
- 70 tapered sperm cells
- 45 pyriform sperm cells

- 52 amorphous sperm cells
- 15 small sperm cells
- 2 round sperm cells



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### General Ideas of Our Framework

- Use of color space combinations
  - RGB withdraws: high correlation among components, no representation of color differences in uniform scale
  - RGB + YCbCr + L\*a\*b\*: intensity and chromatic components easily and independently controlled
  - L\*a\*b\*: perceptual uniformity, efficient in measurement of small color differences (Euclidian distance)
  - YCbCr: Euclidian distance for color space
- Use of clustering method
  - k-means : illumination variation problem
- Identification of sperm head direction



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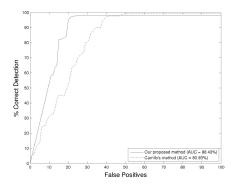


#### Our Results

We compare our results with Carrillo et al. (2007) and use TP, FP and Precision as evaluation metrics.

	Our proposed method	Carrillo's method
Precision	97,6%	95,7%
True Positives (TP)	205	201
False Positives (FP)	23	39

#### Our Results

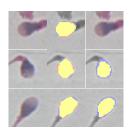


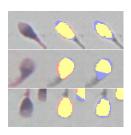
ROC curves for sperm head detection. Detection rate and number of false positives according to the results of our proposed method (continuous line) and Carrillo's method (dotted line), versus hand-segmented masks.

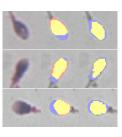
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#### Our Results





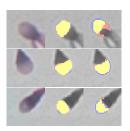


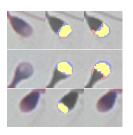
Results of head segmentation. We show representatives for best results (left section), center section for average results, and right section for worst results. For each section, we present the original (first column), our result (second column) and Carrillo's method result (third column). The blue color represents the gold-standard, red presents our proposed/Carrillo's method and yellow the overlap between gold-standard and our proposed/Carrillo's method.

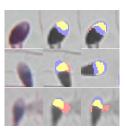
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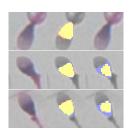


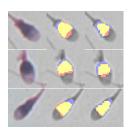


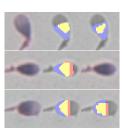


Results of acrosome segmentation. We show representatives for best results (left section), center section for average results, and right section for worst results. For each section, we present the original (first column), our result (second column) and Carrillo's method result (third column). The blue color represents the gold-standard, red presents our proposed/Carrillo's method and yellow the overlap between gold-standard and our proposed/Carrillo's method.

#### Our Results





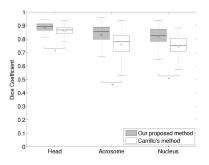


Results of nucleus segmentation. We show representatives for best results (left section), center section for average results, and right section for worst results. For each section, we present the original (first column), our result (second column) and Carrillo's method result (third column). The blue color represents the gold-standard, red presents our proposed/Carrillo's method and yellow the overlap between gold-standard and our proposed/Carrillo's method.

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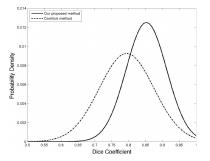


#### Dice Coefficient



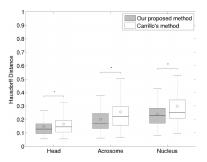
Dice coefficient for head, acrosome and nucleus. On each box, the edges are the 25th and 75th percentiles and the whiskers extend to the most extreme data points that are not outliers. For each box, we show the median value (horizontal line) and the sample mean ( $\circ$ ). Statistically significant differences between our proposal (grey) and Carrillo's method (white) using Wilcoxon rank sum test are indicated (\*p < 0.05).

#### Dice Coefficient



Probability density function for Dice coefficient. Acrosome, nucleus and sperm head segmentation results are showed together, considering the Dice coefficients achieved by our proposed method (continuous line,  $\mu=0.85\pm0.0026,\ s^2=0.0036$ ) and by Carrillo's method (dotted line,  $\mu=0.79\pm0.0035,\ s^2=0.0065$ ).

#### Hausdorff Distance

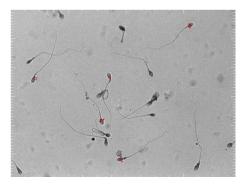


Hausdorff distance for head, acrosome and nucleus. On each box, the edges are the 25th and 75th percentiles and the whiskers extend to the most extreme data points that are not outliers. For each box, we show the median value (horizontal line) and the sample mean ( $\circ$ ). Statistically significant differences between our proposal (grey) and Carrillo's method (white) using Wilcoxon rank sum test are indicated (\*p < 0.05).

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### Characterization of Sperm Heads

 Use of active contours to generate parametrized curves (AC parameters according to number of inflexion points)



## Characterization of Sperm Heads

- Histogram of orientations from parametrized contours
- Chain code from parametrized contours
- Histogram of normalized curvatures + clustering
- Shape features from curves: ellipseness and bottleness

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## Classification of Sperm Heads

- Gold-standard for sperm head classification
- Two-class problem to start: normal and abnormal sperm heads
- Multiple-class problem: normal, pyriform, tapered, round and amorphous sperm heads
- Evaluation of 3 classifiers: Bayesian, MLP, SVM

## Summary

 Our work is aimed to propose a novel methodology to accurately characterize sperm components to facilitate the subsequent morphological sperm analysis with results similar to those of referent international experts in the field, focusing on a depth analysis of abnormal sperm for fertility diagnosis, prognosis, reproductive toxicology, basic research or public health studies.

## Summary

- So far, we built a gold-standard for head sperm parts segmentation, with the cooperation of an expert.
- Also, we have developed an improved two-stage framework for detection and segmentation of human sperm head characteristics using color space combinations together with a clustering method, outperforming the-state-of-the-art method.
- Now, our work is focused in the characterization stage (and later the classification stage), and our main goal is the formulation of a new descriptor for sperm heads which will permit classifying them among a wide variety of head shapes.

