This MICCAI paper is the Open Access version, provided by the MICCAI Society. It is identical to the accepted version, except for the format and this watermark; the final published version is available on SpringerLink.

Supplementary material - A Novel Semi-Supervised Approach for Red Blood Cell Shape Analysis in Flow

Andrea Caputo[1,2][0009−0003−7788−8829]✉, Lars Kaestner[2,3][0000−0001−6796−9535], and Stephan Quint[1][0000−0003−4412−7559]

[1] Cysmic GmbH, Saarbrücken, Germany
andrea.caputo@cysmic.de
[2] Dynamics of fluids, Saarland University, Saarbrücken, Germany
anca00013@uni-saarland.de
[3] Theoretical Medicine and Biosciences, Saarland University, Homburg, Germany

S1 Contouring method

As stated in Section 2.1, our contouring method involves two NNs designed to select the right contour starting from the middle output of CPSAM [1]. In Table S1, the detailed architectures of both models are shown. The entire pipeline was trained to identify the best-fitting contour for each cell on a labeled dataset comprising 3 contour categories (i.e. *not valid*, *sub-optimal*, *optimal*). After training, our contouring method correctly selects the *optimal* contour in 82% of cases on the validation set. If we consider both the *optimal* and *sub-optimal* contours as acceptable selections, the accuracy increases to 98%.

Table S1. Architectures of the Filter Model and Ranker Model. The arrow denotes a linear layer; BN denotes batch normalization; DO denotes dropout; and LN denotes layer normalization.

Stage	Filter Model	Ranker Model
Block 1	$d = 15 \rightarrow 64$, BN, GELU, DO(0.2)	$d = 15 \rightarrow 32$, LN, ReLU, DO(0.15)
Block 2	$64 \rightarrow 32$, BN, GELU, DO(0.2)	$32 \rightarrow 16$, LN, ReLU
Block 3	$32 \rightarrow 16$, GELU	–
Output	$16 \rightarrow 1$	$16 \rightarrow 1$

S2 Input vector structure

An overview of the features we used to build the 22D input vector to our clusterer, grouped by category, is presented here:

– **Basic geometric descriptors:** eccentricity; circularity; aspect ratio; ratio of the maximum to minimum Feret diameters; sum of the first 5 amplitudes

(from the 1^{st} to the 5^{th}) of the Fourier transform (FT) of the Feret profile, normalized by the DC component; maximum symmetry value; average symmetry value; distortion projection index (i.e., a flow-aware version of the eccentricity)

- **Convexity-based descriptors:** convexity; solidity; ratio of the maximum to minimum Feret diameters of the convex hull; sum of the first 5 amplitudes (from the 1^{st} to the 5^{th}) of the FT of the Feret profile of the convex hull, normalized by the DC component; the first 2 amplitudes (1^{st} and 2^{nd}) of FT of the Feret profile of the convex hull
- **Curvature-based descriptors:** mean curvature value; curvature complexity (i.e., amplitude of the most dominant peak of the curvature FT normalized by the DC component); area under the curve of the curvature autocorrelation; number of lags (i.e., steps) after which the autocorrelation drops below $\frac{1}{e}$; the first 2 amplitudes (1^{st} and 2^{nd}) of the curvature FT; curvature autocorrelation value considering a single lag (i.e., point-to-point continuity of the curvature profile); ratio between high (from the 5^{th} to the 9^{th}) and low (from the 1^{st} to the 4^{th}) amplitudes of the curvature FT

References

1. Pachitariu, M., Rariden, M., Stringer, C.: Cellpose-sam: superhuman generalization for cellular segmentation. bioRxiv (2025), https://www.biorxiv.org/content/early/2025/05/01/2025.04.28.651001