

Somatic Cell Count in Buffalo Milk using Fuzzy Clustering and Image Processing Techniques

Aline Silva Ramos, Cristiano Hora Fontes, Adonias Magdiel Ferreira, Camila Costa Baccili, Karen Nascimento da Silva, Viviani Gomes, Gabriel Jesus Alves de Melo

SUPPLEMENTARY FILE

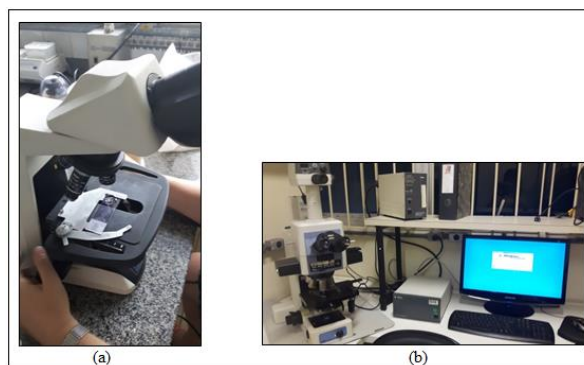


Fig. S1. (a) Observation of the slides in an optical microscope and (b) Image acquisition system

Table S1. Number of images in each cluster (FCM method)

Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
84	108	130	127	62

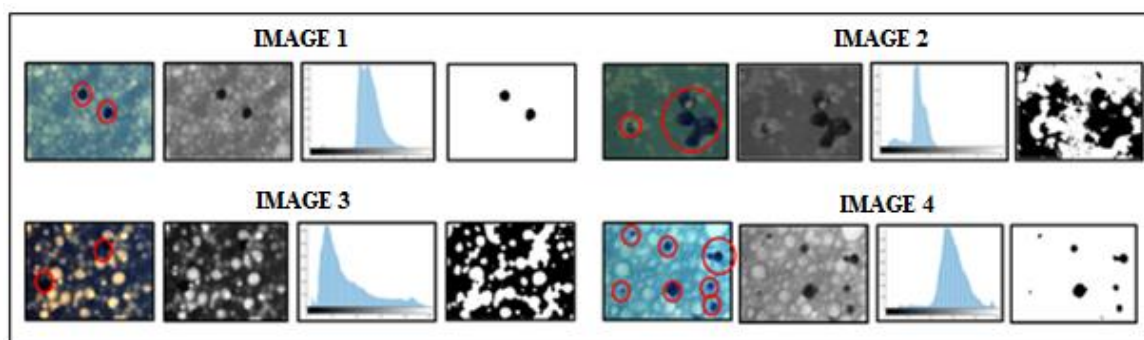
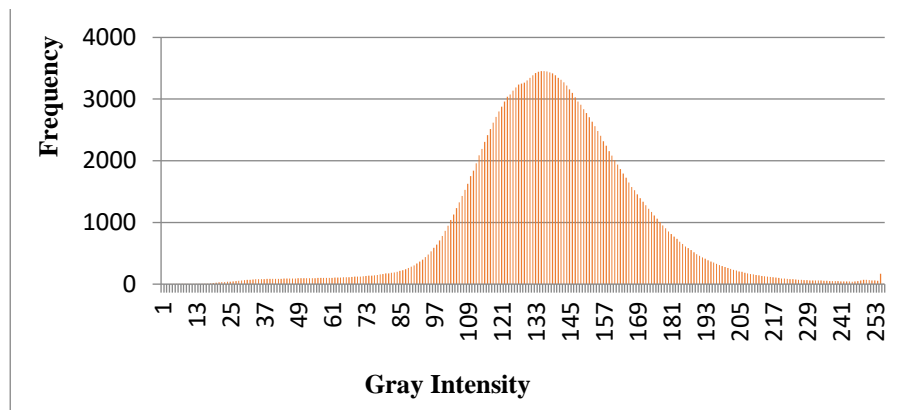
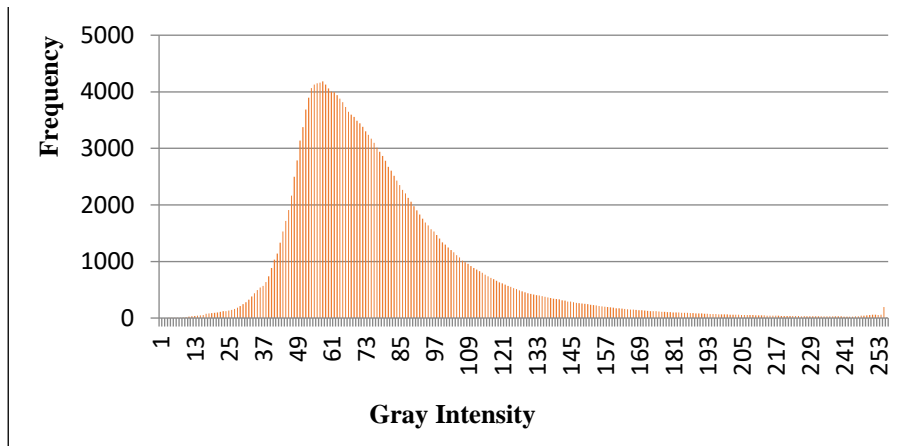


Fig. S2. Different images processed with the same threshold. In two images (2 and 3) the segmentation did not perform well since parts of the image background were identified as objects (cells). Images 1 and 4 show similarity in background tone and were segmented correctly

Table S2. Counting results - proposed method (SCCFCI) and traditional approach (DMSCC)

SCCFCI		CCS (without previous fuzzy clustering)		DMSCC		
Melo	Rosin	Melo	Rosin	Expert 1	Expert 2	Expert 3
1476	3838	2235	7473	1475	1507	1510



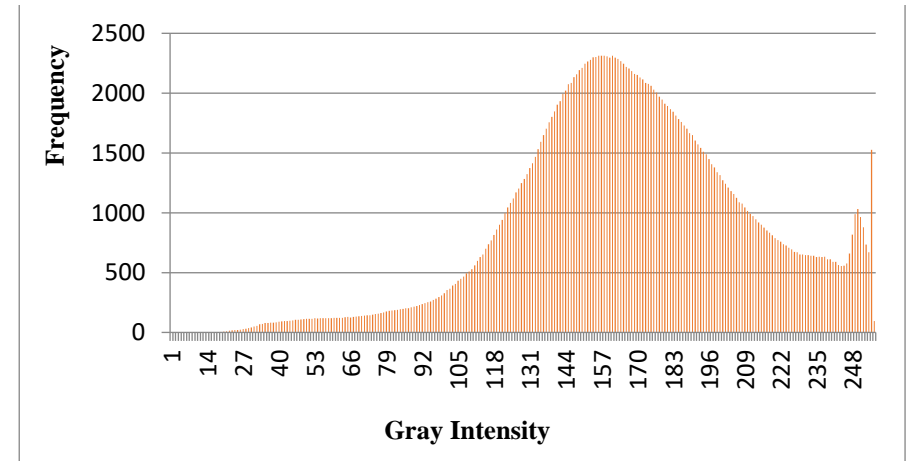
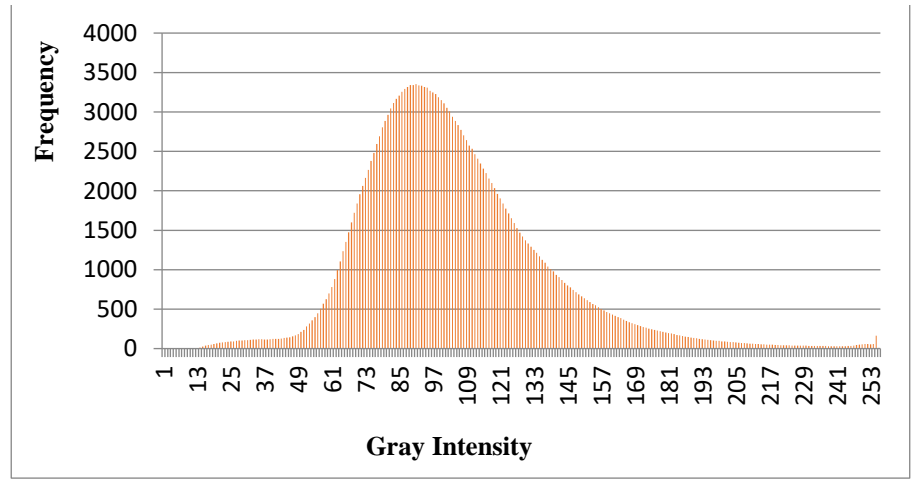
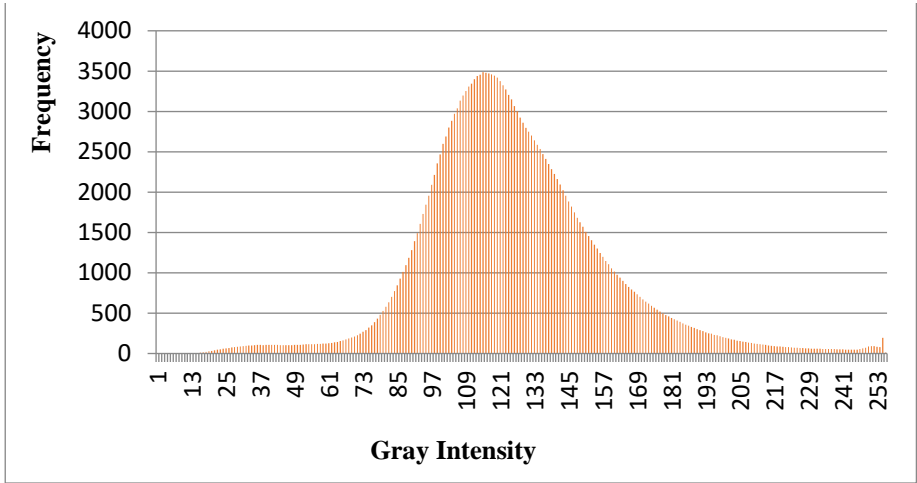
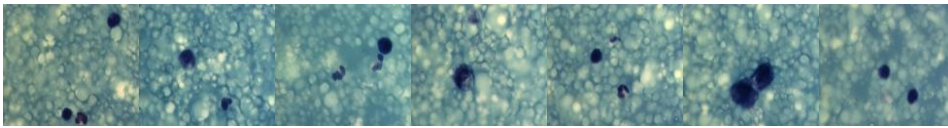


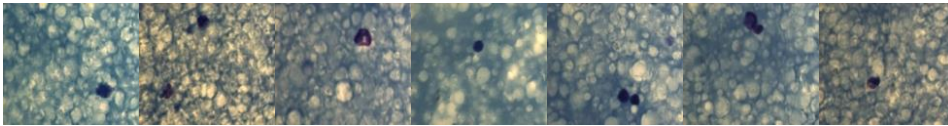
Fig. S3. Histograms associated with each center/pattern



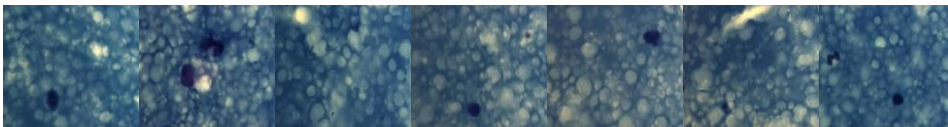
Cluster 1



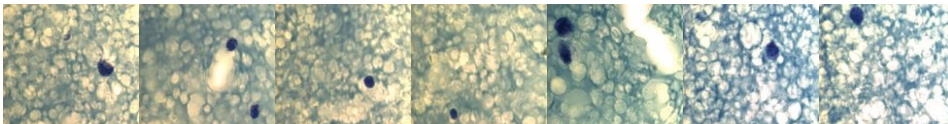
Cluster 2



Cluster 3



Cluster 4



Cluster 5

Fig. S4. Some images of each of the recognized clusters

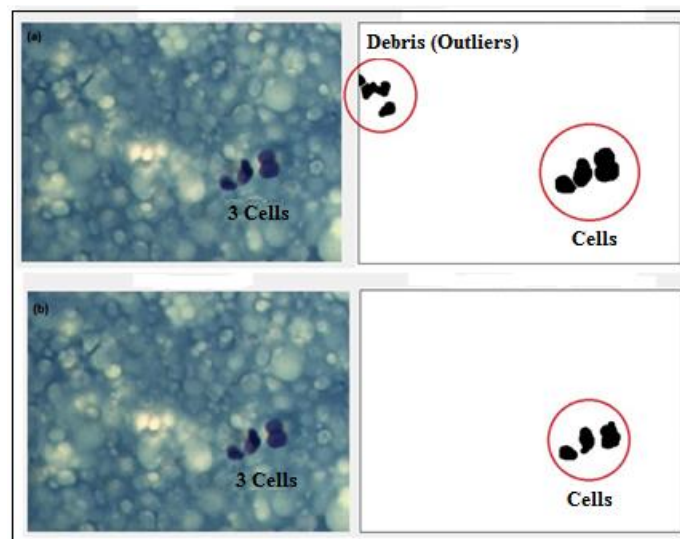


Fig. S5. The same original image – a) Rosin method, b) Melo method

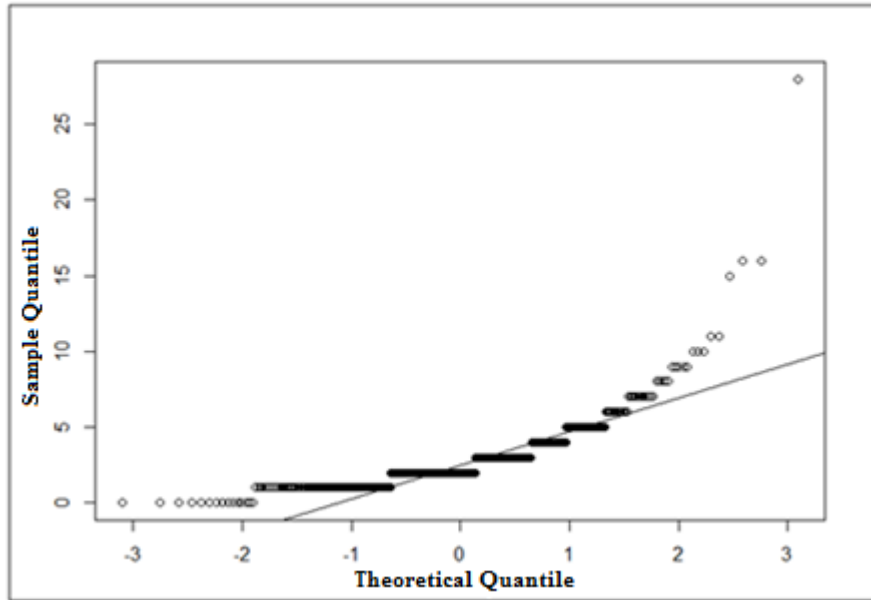
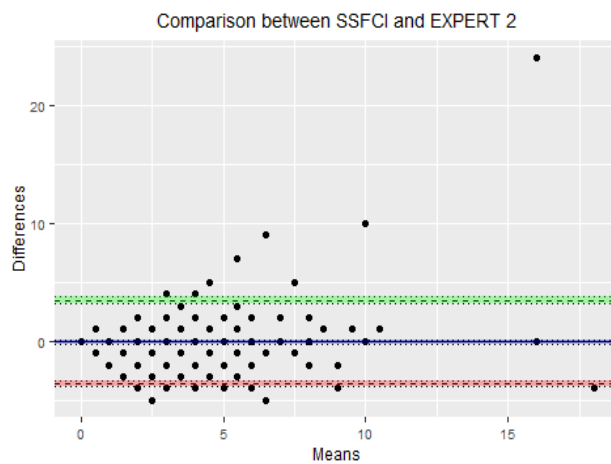
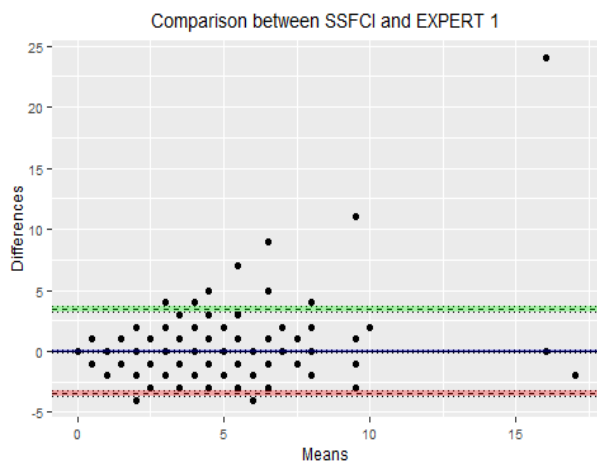


Fig. S6. Normal distribution test – distribution of cell counts in all images (SCCFI)

Table S3. Spearman's correlation test

		DMSCC		
	SCCFI	Expert 1	Expert 2	Expert 3
SCCFI	1	0.753	0.738	0.721
Expert 1	0.753	1	0.938	0.955
Expert 2	0.738	0.938	1	0.956
Expert 3	0.721	0.955	0.956	1



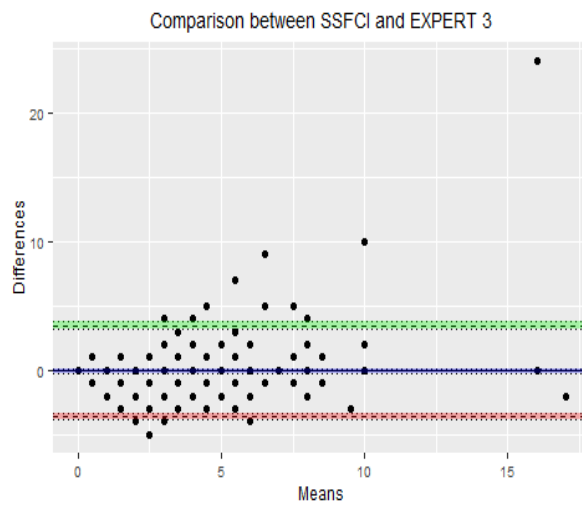


Figure S7. Bland-Altman plots - Similarity between counts obtained by the proposed method and by experts.

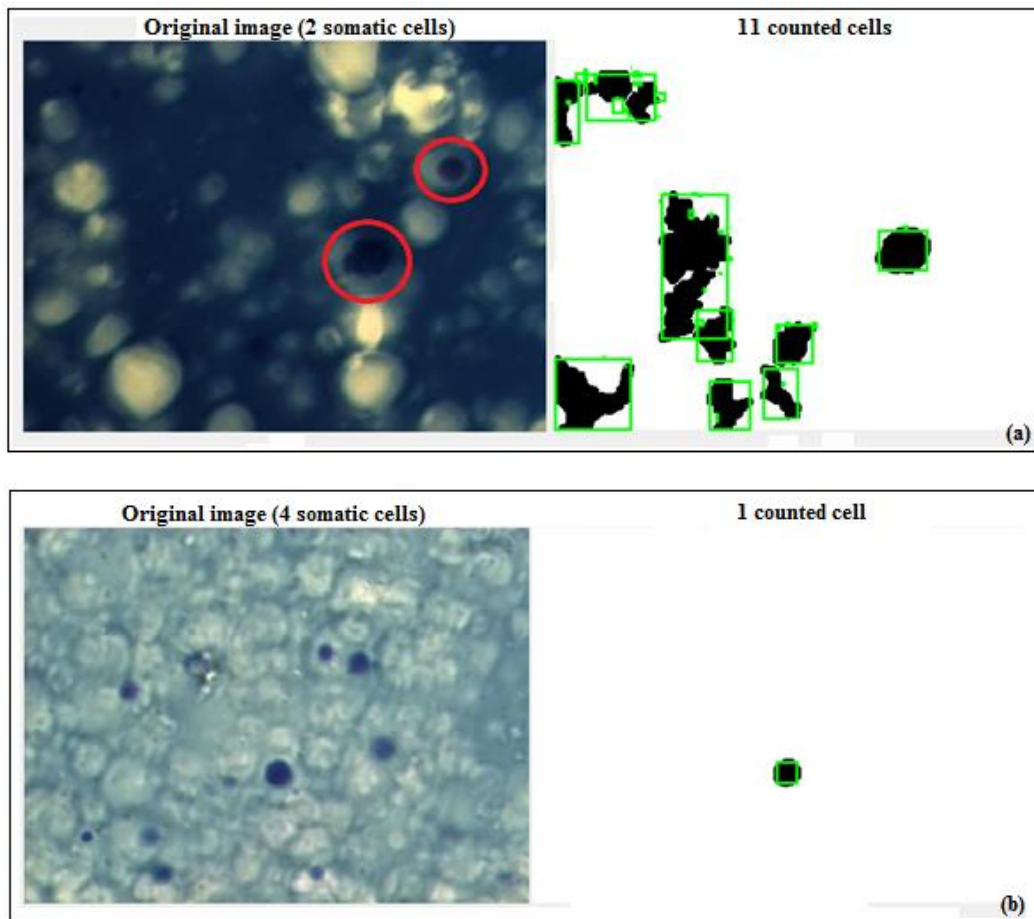


Figure S8. a) Very dark image, b) Sample with excess fat