function [features, featureMetrics] = customParasitologyFcn(I)

persistent targetImage

matchHistograms = true; %Low-cost way to improve performance

% Histogram matching may help!

if isempty(targetImage) && matchHistograms

targetImage = rgb2gray(imread('C:\Users\Bhavana\Documents\MATLAB\FinalCode\

BloodCellAnalysis\BloodSnearImages\img19.jpg'));

end

extractorMethod = 'SURF'; %#ok Auto;BRISK;FREAK;SURF;BLOCK

% Convert I to grayscale if required.

[height,width,numChannels] = size(I);

if numChannels > 1

grayImage = rgb2gray(I);

else

grayImage = I;

end

if matchHistograms

grayImage = imhistmatch(grayImage,targetImage);

end

gridStep = 8;

gridX = 1:gridStep:width;

gridY = 1:gridStep:height;

[x,y] = meshgrid(gridX, gridY);

gridLocations = [x(:) y(:)];

[features, scenePoints] = extractFeatures(grayImage,gridLocations,...

'Method',extractorMethod,...

'SURFSize',64,...

'Upright',true);

try

features = double(features);

catch

features = double(features.Features);

end

featureMetrics = var(features,[],2);