Evaluating the Quality of Salvaged Blood Products Using Stimulated Raman Spectroscopy and Deep Learning

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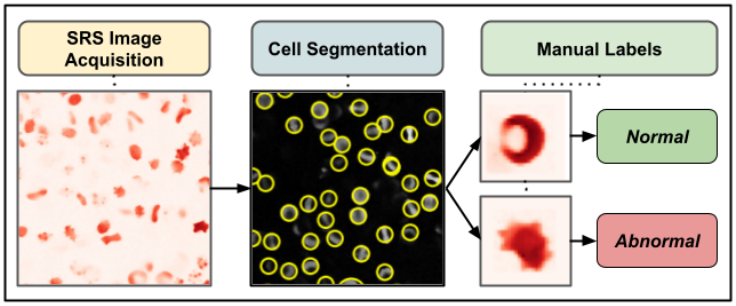
Background. Autologous blood salvage in surgery is common, but its benefits are unclear for spinal deformity surgery. In an ongoing prospective trial at our institution, we observed that salvaged blood has elevated hemolysis index (HI) and plasma free hemoglobin compared to pre-operative baseline blood samples, suggestive of red blood cell (RBC) damage during salvage processing. Evaluation of blood product quality would allow clinicians to determine if salvaged blood is safe to transfuse. However, long turnaround times preclude the use of traditional lab-based assays for intra-operative decision making. Stimulated Raman spectroscopy (SRS) enables rapid intra-operative microscopy of tissue samples, producing digital images that can be analyzed using computer vision techniques. SRS images showed differences in RBC morphology between baseline and salvaged blood. As there are more than 10,000 RBCs in each image, manual cell-level quantitative analysis is impractical. We hypothesize a deep-learning approach to quantify RBC morphology in baseline and salvaged blood would enable timely evaluation of blood product quality.

Methods. 20 baseline and 16 salvaged blood samples were obtained from patients undergoing spinal deformity surgery and imaged with the NIO SRS platform. Over 350,000 RBCs were segmented using Laplacian of Gaussian blob detection (*fig. I*), and we pre-trained a Resnet50 feature extraction network using SimCLR self-supervision. A binary classification head was fine-tuned using 7,500 hand-labelled images to predict normal (biconcave disk) vs abnormal RBC morphology. To show concordance with lab-based assays, we trained a regression model to predict mean corpuscular volume (MCV) and red cell distribution width (RDW) from sample mean RBC feature embeddings.

Results. Our fine-tuned model achieved a **mean accuracy of 0.856±0.004** and **AUC-ROC of 0.908±0.005** for the cell-level morphologic classification task across five cross-validation splits. TSNE of the pre-trained RBC feature space revealed neighborhoods of RBCs with similar morphology (*fig. II*). Random forest regression predicted MCV and RDW within 6% of lab-obtained values. Salvaged samples had a higher proportion (25%) of abnormal RBCs than baseline samples (11%).

Conclusion. Our preliminary results demonstrate the use of deep learning to enable high-throughput morphologic analysis of RBCs in blood samples. A larger sample and comparison with lab-based metrics for hemolysis and cellular damage are necessary to evaluate blood product quality. Ongoing work aims to develop and validate a distance-based metric to compare baseline and salvaged blood samples based on RBC morphology and predict post-operative complications.

Figure I: Building a dataset of individually segmented red blood cells



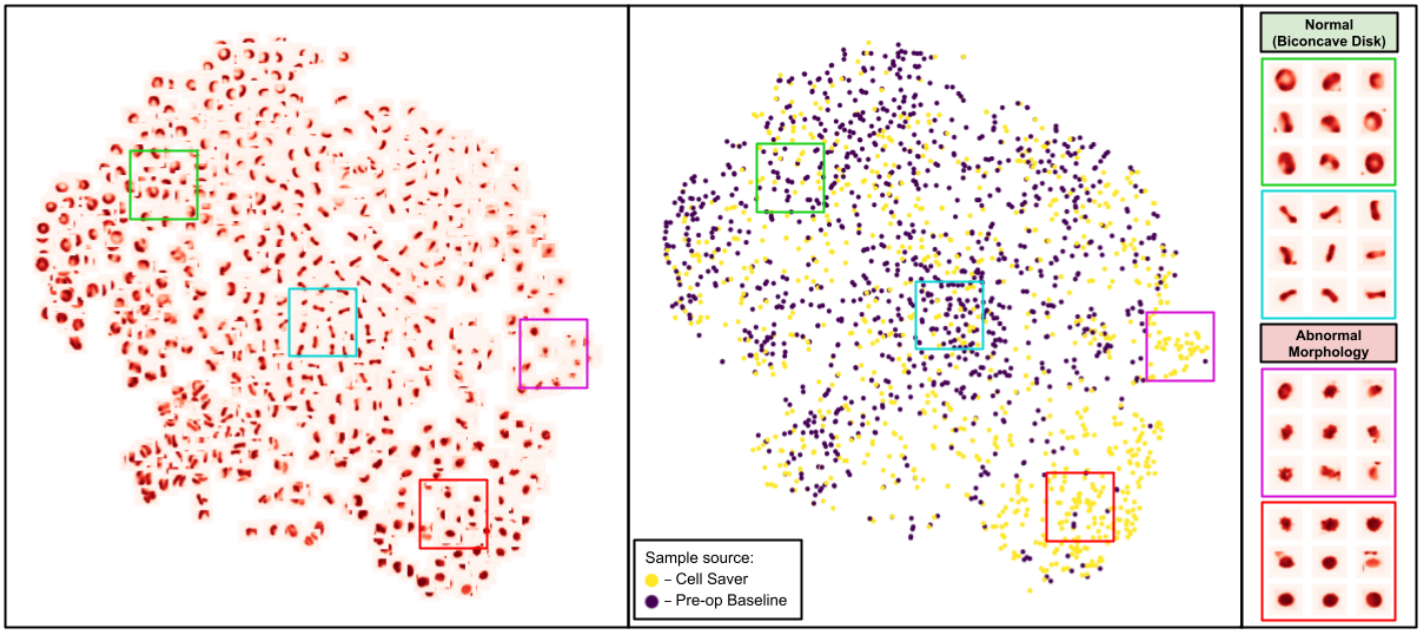


Figure II: TSNE plots of encoded RBC feature maps. Images (*left*); blood sample category and example regions of similar RBC morphology (*right*).