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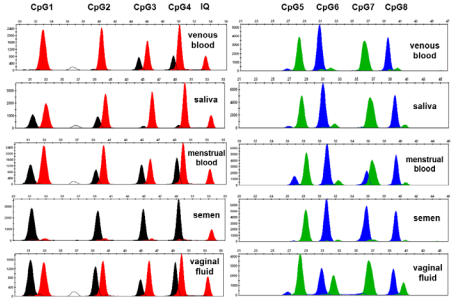
Construction and evaluation of in-house methylation-sensitive SNaPshot system and three classification prediction models for identifying the tissue origin of body fluid

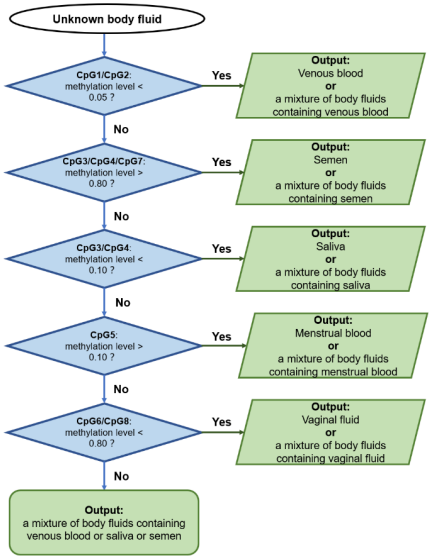
Key words: DNA methylation, Body fluid, Forensic identification, SNaPshot, Machine learning

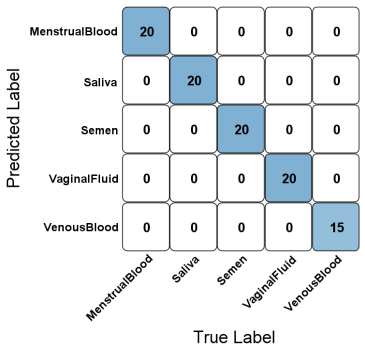
Research Summary

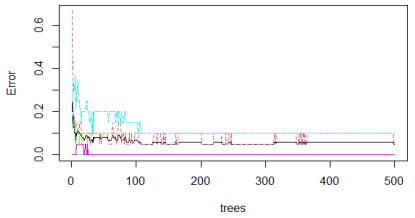
This study focused on the application requirement of tissue origin identification of five common body fluids in forensic medicine, constructed and validated based on eight novel body fluid-specific DNA methylation markers:



- **A methylation-sensitive SNaPshot system**
- **An artificial body fluid prediction model**
- **Support vector machine learning prediction models**
- **A random forest machine learning prediction model**







Innovation points

- **The results indicated that the in-house system showed good species specificity, sensitivity (0.5 ng) and ability to identify mixed biological samples..**

- **For five common body fluids (venous blood, semen, vaginal secretion, saliva, and menstrual blood), the accuracy of the prediction model based on researcher's experience was 95.8%; the prediction accuracy of the SVM prediction model was 100% for all kinds of body fluids except saliva (96.84%); and the prediction accuracy of the RF prediction model was 100% for all five kinds of body fluid.**