



# Master Forensic Science

Research Projects 2019-2020





# Research projects 2019-2020

The University of Amsterdam's (UvA) Master's programme in Forensic Science, offered by the Faculty of Science, is unique in the Netherlands. The programme distinguishes itself from most international Master's programmes in Forensic Science by building on a range of scientific disciplines, such as Chemistry, Computer Science, Life Sciences, Mathematics, Physics, and other exact sciences. The goal of the programme is to train good scientists, armed with forensic knowledge and skills.

A part of the curriculum is a six-month internship during which scientific research is executed that is relevant to the forensic field. This document gives an overview of the capabilities of our students and the many ways in which a research project can be conducted.

For more information please contact:  
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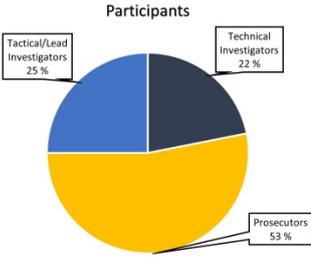
Title	Organisation	Student	Previous education
<b>Criminalistics</b>			
Quantifying the interpretation of value of evidence within the Finnish criminal justice system	National Bureau Of Investigation Forensic Laboratory, Finland	Verna Kulomaa	Analytical Chemistry
Creating and testing an impact analysis for Rapid DNA technologies for the Dutch Criminal Justice System	Forensische Opsporing Midden Nederland	Merel van Cooten	Health Sciences
Decision-making processes during trace recovery	Nederlands Forensisch Instituut(NFI)	Katharina Draxel	Biological Sciences
<b>Digital Forensics</b>			
Ground Truth Labeling of Digital Traces for Neural Networks	NFI	Ameya Puranik	Electronics and Telecommunication Engineering
Application of Deep learning neural networks and techniques for person Re-Identification in forensics	NFI	Aida Ploco	Computer Science
Face Morphing Detectin	NFI	Ilias Batskos	Electrical and Computer Engineering
<b>Forensic Biology</b>			
The genetic pawprint: Identification and matching of dogs based on genetic marker data in forensics and breeding strategies	University Utrecht	Citlalli Limpens	Microbiology
Variation in body fluid specific mRNAs: can cell type and donor be associated?	NFI	Simao Ribeiro Margarido	Forensic Science
Characterization of length and sequenced based allele frequencies for previously uncharacterized subpopulations of Canada	University of Toronto, Canada	Loes Steller	Biomedical Sciences
Identification of age informative gender specific DNA methylation markers – A proof of concept study	University of Amsterdam (UvA)	Zhong Wan	Biotechnology
<b>Forensic Biophysics</b>			
Photogrammetry combined with thermal imaging to document crime scenes and estimate post-mortem interval	Amsterdam Universitair Medisch Centrum (UMC)	Maarten Willekers	Medical Natural Sciences

Title	Organisation	Student	Previous education
<b>Forensic Chemistry</b>			
Enzyme degradation of nitrocellulose with LC-MS/ELSD	UvA	Courtney Dickson	Biology
The use of portable NIR spectroscopy and chemometrics for detection and identification of bulk explosive substances pre-explosion	Nederlandse Organisatie voor toegepast-natuurwetenschappelijk onderzoek (TNO)	Floor Dussel	Molecular Life Sciences
Optimisation of a non-targeted HPLC-HR-QToF-MS/MS method for the analysis of forensic samples of new psychoactive substances	University of Lausanne, Switzerland	Sofie Huisman	Liberal Arts and Sciences, major Chemistry
Crowbar Paint Project	Institute of Environmental Science and Research (ESR), New Zealand	Alica Kandler	Forensic Science
Assessment of risk and injury potential during ATM bombings	UvA	Frederike Oetker	Science Communication and Bionics
ETN IRMS Project	NFI	Roos Hessels	Earth Science (Geology)
Chemical profiling of fentanyl in complex matrices	TNO	Djarah Kleiweg	Life Science & Technology
Socio-economic changes in wastewater: licit and illicit drug use patterns in Barcelona and Lleida	Catalan Institute for Water Research, Spain	Nicole Schröter	Chemistry
<b>Forensic Medicine</b>			
Multi-factorial forensic age estimation: Combining radiographs of the third molars, the left wrist and both clavicles	Ghent University, Belgium	Heleen Coreelman	Biochemistry and Biotechnology
Evaluating the value and role of (preliminary) DECCA advice in physical child abuse assessment by the Netherlands Forensic Institute	NFI	Nina Eckhardt	Psychobiology
Extraction of Surface and Internal Fingerprints from Optical Coherence Tomography Scans for Forensic Identification	Amsterdam UMC	Lisa Klok	Medical Sciences and Technology
Forensic and epidemiological analysis of decomposed bodies in Catalonia	Universitat Autònoma de Barcelona, Spain	Karin Körsegaard	Gene Technology
Using Surface Plasmon Resonance to determine the age of deposited body fluids	Amsterdam UMC	Lisanne Limburg	Psychobiology
Determining the age of bones with fluorescence spectroscopy	Amsterdam UMC	Daphne Muijderman	Biomedical Sciences
Age estimation of human biological traces - Identifying important chemical biomarkers	Vrije Universiteit (VU)	Jacky Haring	Chemistry

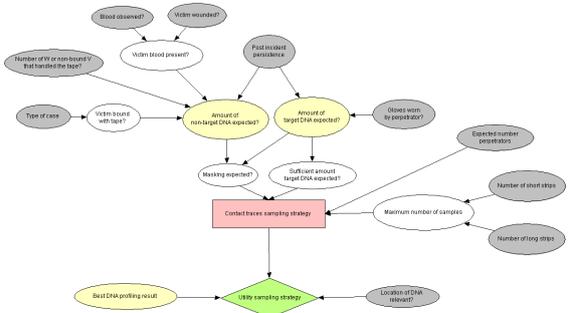


Title	Organisation	Student	Previous education
<b>Forensic Medicine</b>			
What is the value of the physical investigation that is done in child sexual abuse cases?	NFI	Annabelle Kuipers	Health and Life Sciences
<b>Forensic Physics &amp; Forensic Chemistry</b>			
LC-MS analysis of IBNS inks on euro currency	UvA	Alissa Sczyslo	Biology
<b>Forensic Statistics</b>			
Forensic Evaluation of Objective Methods for Automated Analysis of Glock Cartridge Case Marks	NFI	Jorit Delen	Mathematics and Applications
Common Source versus Specificic Source approach for automated comparison of Glock cartridge case marks	NFI	Jeroen Letteboer	Physics and Astronomy
<b>Other</b>			
Validating the Authenticity of 17th Century Royal Clothing with the Use of Forensic Techniques	Rijksmuseum, Amsterdam	Luca Cannatella	Evolutionary Biology
Identification of possible human biological traces found on 18th century clothing	Rijksmuseum, Amsterdam	Yoram Goedhart	Psychobiology

## Criminalistics

Student	Verna Kulomaa								
<i>Research carried out at</i>	National Bureau Of Investigation Forensic Laboratory Finland								
<i>Supervisor</i>	Tuomas Salonen MSc								
<i>Title thesis</i>	Quantifying the interpretation of value of evidence within the Finnish criminal justice system								
<p data-bbox="181 495 288 521"><i>Abstract</i></p> <div data-bbox="188 555 719 853">  <table border="1" data-bbox="308 568 619 831"> <caption>Participants</caption> <thead> <tr> <th>Occupation</th> <th>Percentage</th> </tr> </thead> <tbody> <tr> <td>Prosecutors</td> <td>53 %</td> </tr> <tr> <td>Tactical/Lead Investigators</td> <td>25 %</td> </tr> <tr> <td>Technical Investigators</td> <td>22 %</td> </tr> </tbody> </table> </div>	Occupation	Percentage	Prosecutors	53 %	Tactical/Lead Investigators	25 %	Technical Investigators	22 %	<p data-bbox="746 501 1412 1821">A pilot study of a survey-based methodology for measuring understandability of forensic reports from the National Bureau of Investigation Forensic Laboratory of Finland was completed with promising results. As the goal of the study was to measure the understandability of reports themselves rather than an aspect of the reports (such as weak versus strong conclusions), variability was intentionally increased by varying the type of findings (DNA, handwriting), conclusion style (LR based, currently existing styles), strength of the findings (weak, moderate, strong), the order of appearance, and participants in different occupations (prosecutors (n=17), lead and tactical investigators (n=8), technical investigators (n=7)). The main section of the survey included two types of questions: Likert-scale questions, and true-false questions. Likert-scale questions were used to measure the belief-change resulting from reading a report by subtracting the prior belief of the participant from the posterior belief. True-false questions were used to measure the correct understanding of the report. Together these were used to calculate the understandability indices, which were used to assess the differences between conditions and to calculate success rates. The reliability of the survey was assessed with Cronbach's alpha. The over-all alpha for the true-false questions was <math>\alpha=0.65</math>, however lower alpha values were observed when assessing the true-false questions concerning the handwriting report. Misunderstandings seem to occur for a variety of reasons, for example, because of the strength of the findings, the type of findings, and the participant's expectations. For future development of the survey, it is recommended to add another measurement system beside the Likert-scale to measure the belief-change and true-false questions with inverse questions. The knowledge from the pilot study gives direct pointers for the in development of a survey-based tool for measuring report understandability in Finland and should provide a solid foundation for the next survey.</p>
Occupation	Percentage								
Prosecutors	53 %								
Tactical/Lead Investigators	25 %								
Technical Investigators	22 %								

Student	Merel van Cooten
<i>Research carried out at</i>	Forensische Opsporing Midden Nederland
<i>Supervisor</i>	Anna Mapes
<i>Title thesis</i>	Creating and testing an impact analysis for Rapid DNA technologies for the Dutch Criminal Justice System
<p data-bbox="183 465 288 495"><i>Abstract</i></p> 	<p data-bbox="762 472 1407 1827">In this study, we describe the design of a science-based analysis model that allows data collection on the effectiveness of rapid and mobile DNA technologies at the crime scene. Furthermore, it delivered the first step in the data collection, where we tested the influence of the availability of rapid DNA technologies at the crime scene on the type and quality of DNA traces selected for rapid analysis. The analysis model was designed with the EMMIE model as underlying framework for variable selection. The study set-up included an experimental group that will deploy rapid DNA technologies at the crime scene and a control group that will work under standard conditions. This is followed by a qualitative thought experiment ('what if' scenario), where a hypothetical rapid DNA device can be deployed. The study resulted in an analysis model that enables data collection on actual cases through quantitative casefile analysis and qualitative interviews with Scene of Crime Officers (SoCOs) and criminal detectives. To test the model, data was collected from 19 criminal cases in the control condition. In these cases, 376 DNA traces were sent in for analysis, from which 105 (27.9%) met the criteria for rapid analysis. In the 'what if' scenario, 61.0% (64/105) would have been selected for rapid analysis by the SoCO, originating from 13 of the 19 cases. Statistical analysis showed that significantly more perpetrator related traces were selected. Concerning the quality of the selected traces, we showed that – with a sensitivity threshold of 50 pg/uL of the device - 31.7% would produce a false negative result in the rapid DNA device. These traces would yield a DNA result in the laboratory, but would potentially not generate a profile with the less sensitive rapid DNA technology. The study proved that the developed analysis model can be used to generate knowledge on the effectiveness of rapid DNA technologies, which can aid in the formulation of optimal strategies for its (potential) implementation. It is recommended that this analysis model is shared internationally to stimulate standardized data collection across countries.</p>

<b>Student</b>	<b>Katharina Draxel</b>
<i>Research carried out at</i>	NFI
<i>Supervisor</i>	dr. Yvonne van de Wal
<i>Title thesis</i>	Decision-making processes during trace recovery
<p><i>Abstract</i></p> 	<p>Adhesive tape is a common piece of evidence that is used for a wide array of crimes. Its trace examination is a challenging task due to the variety of traces and the complex trace dynamics associated with the tape. Additionally, as the assessment on activity level gains more importance, a different examination would be necessary to provide information on an activity. This trace examination of adhesive tapes involves a multitude of decisions. These decisions can highly influence the outcome of the examination, and optimal decisions have to be made to ensure a successful examination. Interviews with fingermarks and DNA trace examiners and a case file study were conducted to gain insight into the trace examination of adhesive tapes and the involved decisions. The obtained information could be used to model a Bayesian Decision Network (BDN). Such a BDN uses Bayesian decision theory to quantify the desirability of outcomes and calculate the optimal decision based on data. In this study, a BDN was constructed for the decision of the sampling strategy for contact traces of DNA trace examiners. It visualizes the influences for the decision and provides the optimal sampling strategy under different case circumstances. This is based on success rates and the utilities assigned to the outcomes. Additionally, the network can account for the differences in sampling for source and activity level questions. Therefore, the analysis of a decision using a BDN facilitates simplifying complex decisions and making rational decisions based on data. For that reason, it can be used to optimize protocols for the examination of forensic evidence.</p>

## Digital Forensics

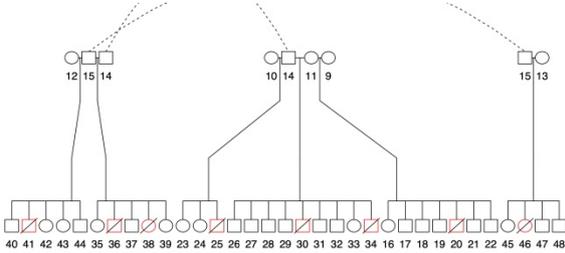
<b>Student</b>	<b>Ameya Puranik</b>
<i>Research carried out at</i>	NFI
<i>Supervisor</i>	ir. Ruud S Schramp
<i>Title thesis</i>	Ground Truth Labeling of Digital Traces for Neural Networks
<i>Abstract</i>	<p>The volume of digital data in an investigation poses a significant problem in digital forensics. There is a need for better methods not only for identifying the relevant traces but also understanding the identified traces on an activity level. Semantic labels can be useful for mapping digital traces to user actions. This work uses data from android devices to test methods for labeling that map digital traces to user actions. A toolkit for acquiring data needed for labeling, a toolkit for labeling using ontology and a named entity recognition based model are developed as part of this research.</p>

Student	Aida Ploco
Research carried out at	NFI
Supervisor	Andrea Macarulla Rodriguez
Title thesis	Application of Deep learning neural networks and techniques for person Re-Identification in forensics
<p data-bbox="185 622 288 651"><b>Abstract</b></p> <div data-bbox="185 658 941 1142"> </div> <p data-bbox="432 1153 730 1182">Spatial-Temporal Distribution</p> <div data-bbox="193 1182 882 1657"> </div>	<p data-bbox="987 622 1407 1805">State-of-the-art person re-identification (ReID) models use Convolutional Neural Networks (CNN) for feature extraction and comparison. Often these models fail to recognize all the intra- and inter-class variations that emerge in person ReID, making it harder to discriminate between people. One idea to reduce these problems and improve performance is by combining two state-of-the-art models. The Omni-Scale Network (OSNet) is used as CNN to test the Market1501 and DukeMTMC-ReID datasets for person ReID. To fully utilize the potential of these datasets, the spatial-temporal constraint is applied, which extracts the camera ID and timestamp from each image to form a distribution. By combining these two methods a hybrid model is created titled Spatial-Temporal Omni-Scale Network (st-OSNet). This model attains a Rank-1 (R1) accuracy of 98.2% and mean average precision (mAP) of 92.7% for the Market1501 dataset. For the DukeMTMC-reID dataset it achieves 94.3% R1 and 86.1% mAP, hereby surpassing the results of OSNet by a large margin for both datasets (94.3%, 86.4%, 88.4%, 76.1%, respectively).</p>

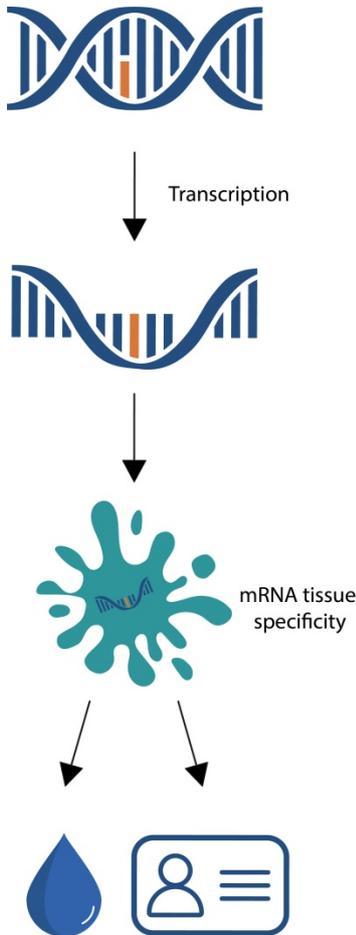


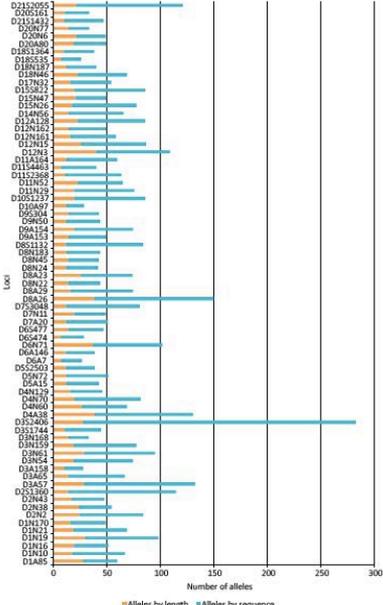
<b>Student</b>	<b>Ilias Batkos</b>
<i>Research carried out at</i>	NFI
<i>Supervisor</i>	Andrea Macarulla Rodriguez
<i>Title thesis</i>	Face Morphing Detection
<i>Abstract</i>	<p>Some countries allow citizens to provide printed copies of face ID photographs in order to issue electronic Machine Readable Travel Documents (e-MRTD). This allows an individual with image manipulation skills to create a novel photograph by blending the photographs of two different individuals before submitting the photograph to the authorities. Depending on the initial similarity of the two morph contributors and the skills of the morph creator, the new photograph can be mistaken for either of the contributors and a legitimate e-MRTD can be issued. The e-MRTD can then be used by either contributor, bypassing automatic face verification systems. For the purpose of this Thesis, a novel detection method was developed, that is not based on detecting morphing traces but rather on quantifying the perceived similarity of two faces and classifying them as a genuine or non-genuine pair. The method was tested on a newly created morph database with realistic case scenarios, and correctly classified non-genuine pairs with a Recall rate of 95%.</p>

## Forensic Biology

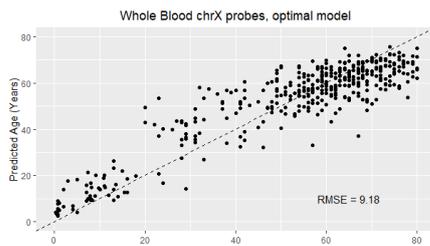
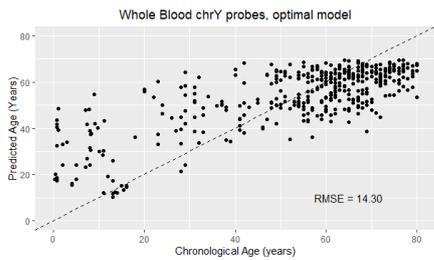
Student	Citlalli Limpens
<i>Research carried out at</i>	Utrecht University
<i>Supervisor</i>	dr. Hille Fieten
<i>Title thesis</i>	The genetic pawprint: Identification and matching of dogs based on genetic marker data in forensics and breeding strategies
<p data-bbox="185 533 288 560"><i>Abstract</i></p>  <p data-bbox="185 1104 772 1290">Full sibship of the largest family line of dogs euthanized due to aggressive behavior. Red blocks represent aggressive dogs, diagonal lines represent dead animals. This pedigree analysis was used for the calculation of the heritability of aggression in the breed.</p>  <p data-bbox="185 1816 746 1877">A Kooikerhondje, Dutch dog breed used as a model in this study.</p>	<p data-bbox="799 542 1410 1760">Due to the popularity of dogs as pets, their involvement in crime and law enforcement seems inevitable. Laws regarding dogs involve animal abuse, bite incidents, and animal welfare regarding their breeding. This study aimed to analyze a Dutch dog breed, to assess animal health and welfare in their breeding, behavioral problems, and general population genetics for the future implementation of a dog DNA database for forensic use in the Netherlands. This was achieved by calculating relevant population parameters such as coefficient of inbreeding, effective population size, breed-related disease incidence, longevity and common causes of death, heterozygosity, and behavioral-traits heritability from a pedigree dataset from the full breed's history. All of this was done with bioinformatic tools developed in a reproducible and adaptable manner to be used in any other dog pedigree and SNP dataset. The coefficient of inbreeding of the Dutch breeds was significantly higher than the average dog population, however no signs of inbreeding depression were found when analyzing reproductive parameters in the breeds. When it comes to diseases, an increased incidence of kidney problems was found in the Dutch Kooiker breed, as well as a high percentage of animals euthanized due to unwanted aggressive behavior. The heritability for the aggressive behavior was calculated, yielding the conclusion that the trait is indeed inheritable, however further behavior phenotypification is needed to assess the genetic attribution of the trait. Furthermore, differences in SNP nomenclature prevented the comparison of data from two different SNP arrays. Consistency will be needed for further analyses between different breeds.</p> <p data-bbox="799 1771 1410 1928">This project gave a preview on the type of information needed for the implementation of a canine DNA database, with an emphasis on dog breeding for healthy animals and prevention of aggression.</p>

<b>Student</b>	<b>Simao Ribeiro Margarido</b>
<i>Research carried out at</i>	NFI
<i>Supervisor</i>	Margreete van den Berge
<i>Title thesis</i>	Variation in body fluid specific mRNAs: can cell type and donor be associated?
<i>Abstract</i>	<p>In recent years, efforts have been made to associate donors with body fluids found on stains. Although it can be easy to do this in single donor samples and in samples with one male and one female donor and only sex specific cells, in other cases it is normally challenging. In the past, four interns at the NFI have contributed to this field of research, with the first investigating six different body fluids as a proof of principle, the following two increasing the discrimination power for blood and semen, and the last one investigating the assays in mixed samples. The aim of this study was to increase the discrimination power for saliva samples by investigating saliva-specific genes. This was achieved by identifying 42 SNPs in 12 saliva-specific genes. A multiplex set was developed on DNA level, achieving a discrimination power of 69%. Twenty-seven of the 42 SNPs were observed in 86 donors and two new SNPs were posteriorly added to the assay, so, in total, 29 SNPs were observed. Although the discrimination power is already relatively high, it might still be possible to increase it by adding new markers. However, it needs to be done carefully, as the addition of markers that might be expressed in other body fluids in addition to saliva might jeopardise the analysis. Two multiplex sets were synthesised for RNA, however, they could not be sequenced upon the submission of this report. The two sets differ by one marker, which was included to understand how it interferes with the other markers. If the extra marker is added the discrimination power drops to 65%, but if not, it drops to 57%. Although the donors (DNA SNPs) and cell type (RNA SNPs) could not be associated in practice, the markers were chosen for their specificity in saliva, so, as a proof of principle, the results are promising for the association of donors to saliva samples. At the moment, donors are being tested on RNA level using two newly developed multiplexes. The next step is to associate those results with the results on DNA level to ascertain if they can in fact be linked.</p>



<p><b>Student</b></p>	<p><b>Loes Steller</b></p>
<p><i>Research carried out at</i></p>	<p>University of Toronto</p>
<p><i>Supervisor</i></p>	<p>dr. Nicole Novroski</p>
<p><i>Title thesis</i></p>	<p>Characterization of length and sequenced based allele frequencies for previously uncharacterized subpopulations of Canada</p>
<p><b>Abstract</b></p>  <p><i>Figure 3. Overview of the number of alleles by length and sequence per locus. The number of length-based variants is shown in orange and the number of additional sequence-based variation is shown in blue for each STR locus included in the 73Plex. These findings are the result of the combined sequencing data from three population groups (African American, Caucasian and Hispanic) and were obtained with the MiSeq Forensic Genomics System.</i></p>	<p>Currently, the “gold standard” for forensic DNA analysis is short tandem repeat (STR) profiling by using polymerase chain reaction (PCR) coupled with capillary electrophoresis (CE). Although this technique is often sufficient for comparisons of DNA samples with one contributor, outcomes of more complex analyses, including DNA mixture deconvolution and indirect genetic kinship analyses, remain inconclusive. Furthermore, interpretation of STR profiling data requires accurate allele frequency tables, and in Canada, allele frequency tables that are used do no longer reflect the current Canadian population. Therefore, the Canadian forensic community identified a research need for complementary tools and up-to-date allele frequency tables that increase the discrimination power of STR profiling for cases in which conventional PCR-CE does not suffice. During recent years, massively parallel sequencing (MPS) has emerged as a valuable tool to increase the discriminatory power of STR analysis. Here, we manually reviewed MPS data from three major population groups (African American, Caucasian and Hispanic) and defined all length- and sequence-based variants. We generated allele frequency tables including 73 new highly polymorphic autosomal STR loci (73Plex) and performed population statistical analyses to provide insights into the current genetic variation of North America’s population groups. The results obtained in this study reveal the amount of sequence-based variation that is captured with MPS in addition to length-based variation and show that the 73Plex contains promising candidates that could improve DNA mixture deconvolution. Finally, our findings show that higher likelihood ratios could be obtained when using MPS data for familial search simulations with distant relatives compared to PCR-CE data, thereby emphasizing the value of including a high number of STR markers and capturing both length- and sequence-based variation.</p>

<b>Student</b>	<b>Zhong Wan</b>
<i>Research carried out at</i>	UvA
<i>Supervisor</i>	dr. Pernette Verschure
<i>Title thesis</i>	Identification of age informative gender specific DNA methylation markers – A proof of concept study
<i>Abstract</i>	<p>Estimation of the age of the unknown DNA-donor from a biological trace is an important and relatively new tool in forensic investigations. Until now, the forensic community has used DNAm markers that were located on autosomal chromosomes, and there has been no research on sex chromosomal DNAm markers. This proof-of-concept research applied the random forest algorithm to build an age-prediction model for forensic investigation purposes that is based on DNAm markers on sex chromosomes. We collected open source datasets containing Infinium 450K DNAm microarray results on sex chromosome of whole blood or buffy coat samples. The model was also built with top 6 autosomal DNAm markers on whole blood and buffy coat datasets from Jana et al., 2017[1] as a comparison with sex chromosome models. The cross-validation process of age prediction using test set returned with a mean root-mean squared error (RMSE) ranging from 7.70 to 14.29 years for models built with sex chromosome probes. As a comparison the RMSE for autosomal models were 5.02 and 6.5 years respectively. Furthermore, extra models were trained with datasets combining six markers on autosomal and sex chromosome probes, a significant decreasing on RMSE were observed ranging from 4.51 to 6.75 years. Only four DNAm markers on the X chromosome from whole blood samples were identified to have a correlation with age. These markers including: DGAT2L6 (cg27064949), PLXNB3 (cg04532200), RPGR (cg01882566) and cg25140188. Age-informative DNAm markers were not identified on Y chromosome. The reduced RFR model built with restricted number of DNAm markers were also constructed, the RMSE were returned ranging from 14.30 to 2.54. Overall, this research indicated some of the age-informative DNAm markers on X chromosomes. The possibility of identifying age-informative DNA methylation markers on Y chromosome remains low. What' more, it is less likely to build an age-prediction model with only sex chromosome DNAm markers as the RMSE was relatively high. A age prediction model built with certain numbers of age-informative markers on sex chromosome and autosomal may provide a higher accuracy comparing to autosomal model in forensic investigation.</p>



Chronological age prediction using 450K methylation probes on X and Y chromosome

## Forensic Biophysics

<b>Student</b>	<b>Maarten Willekers</b>
<i>Research carried out at</i>	Amsterdam UMC
<i>Supervisor</i>	Leah Wilk MSc
<i>Title thesis</i>	Photogrammetry combined with thermal imaging to document crime scenes and estimate post-mortem interval
<i>Abstract</i>	<p>During forensic investigations, finding clues about who might be a possible suspect is one of the main objectives. In- and excluding possible suspects can be done based on the time that has elapsed since a victim deceased, also known as the post-mortem interval (PMI). The current gold standard for PMI estimation is Henssge's nomogram (errors from +- 3 hours when actual PMI is 4hours to +- 10 hours when actual PMI is 24 hours). This method uses rectal and ambient temperature, combined with estimated correction factors to predict the PMI. Potentially, PMI estimation can be improved with the use of the finite difference model created by Wilk et al (2020). This model virtually represents the body as an assembly of small cubes whose change in temperature over time is modelled by using thermodynamic laws, from which PMI can be inferred. The change of body temperature over time depends, amongst other factors, on body posture and contact area between body and environment. Information regarding these two factors can be retrieved from the crime scene by using photogrammetry, a technique which uses a large set of 2D images to construct a 3D-model (point cloud) of a deceased body. To construct a complete point cloud of a deceased body, photographic information should be retrieved from all sides of the body. However, crime scenes tend to be complex in nature, complicating this task for forensic investigators. As a result, it may not be possible to construct a complete point cloud of the body, potentially leading to a change in accuracy of PMI estimations. For the method to be incorporated into forensic practice, it is pivotal to gain insight the errors that may be induced due to the use of incomplete point clouds. The aim of this study is to gain insight into the change in accuracy of PMI estimations induced by a decreased number of images used for point cloud generation. Point clouds were generated by using photographs of 1-4 sides of 5 different deceased bodies. For each of these point clouds, the change of temperature over time was modelled at five different body parts. From this decrease in temperature over time, PMIs were inferred. The point cloud generated with photographs from all sides of the body calculated the accurate PMI, after which point clouds generated with a decreasing number of photographs were than compared to it. Calculated differences in PMI estimations ranged from 0 – 300 minutes when one or two of the possible four sides around the body is used for point cloud generation. In contrast, point clouds generated with photographs from three of the four sides around the body resulted in a difference in PMI of 0 – 100 minutes.</p>

## Forensic Chemistry

<b>Student</b>	<b>Courtney Dickson</b>
<i>Research carried out at</i>	UvA
<i>Supervisor</i>	dr. Bob Pirok
<i>Title thesis</i>	Enzyme degradation of nitrocellulose with LC-MS/ELSD
<i>Abstract</i>	<p>Contemporary forensic analysis of explosives lacks both existing research and innovative methodologies to investigate nitrocellulose - the primary organic propellant in smokeless powders. These powders are commonly found in improvised explosive devices used in criminal activities, including terrorist attacks, which are of preminent concern to societies. This research explores a novel approach to investigating smokeless powders by using enzymes to degrade the nitrocellulose polymer, composed of repeating nitrated monosaccharide subunits. Using an in-solution set-up, the primary objective of this work was to identify and profile nitrocellulose samples. Differential nitration of the monosaccharide subunits in the polymer may give rise to a chemical "fingerprint" of a particular batch of nitrocellulose, such that a nitration profile could be used to link samples of explosives collected in the field to a production batch. Following enzymatic degradation, the resulting products were separated and analysed using LC-ELSD/MS. Results suggested that the enzymatic degradation of nitrocellulose cleaved the polymer at the <math>\beta</math>-1,4-glucoside bond, yielding individual monosaccharide subunits with the potential for nitration profiling. This research presents an encouraging and innovative methodological advancement for the degradation and analysis of nitrocellulose extracted from smokeless powders. Further development in this promising line of scientific enquiry can yield a practicable forensic tool in criminal investigations of explosives.</p>

Student	Floor Dussel
<i>Research carried out at</i>	Nederlandse Organisatie voor toegepast-natuurwetenschappelijk onderzoek (TNO)
<i>Supervisor</i>	Jessica Jansen
<i>Title thesis</i>	The use of portable NIR spectroscopy and chemometrics for detection and identification of bulk explosive substances pre-explosion
<p data-bbox="183 501 288 528"><i>Abstract</i></p> 	<p data-bbox="790 501 1410 2063">Portable NIR spectrometers have high benefits for application in on-scene analyses in the field of forensic science. In this research, the possibilities of the short-wave range (740-1070nm) SciO scanner for classification of pre-blast bulk explosive samples were assessed. A Principal Component Analysis-Linear Discriminant Analysis (PCA-LDA) was made using a dataset of pure energetic materials. It was not possible to correctly classify all energetic materials that were studied, since some samples showed a NIR spectrum of too low quality. All misclassifications from the test datasets were samples with a dark colour or little material. It was not possible to filter this group of samples from the test dataset before they were classified with the PCA-LDA model, which led to several false positive classifications. Nevertheless, the PCA-LDA allowed a true positive classification for 75% of the case samples from the Netherlands Forensic Institute and 94.4% from a dataset of various types and sizes Cyclomethylene trinitramine (RDX) and Octahydro-1,3,5,7-tetranitro-1,3,5,7-tetrazocine (HMX) samples. A true positive classification of the mixture Exan could be made for its component Ammonium nitrate and for the component RDX of Composition C-4. A calculation of the average variance in the projected RDX and HMX test dataset was made. While only one pure compound of both energetic materials was present in the model dataset, the average variance of the RDX samples in the projected dataset was only 1.19 times higher. For HMX, the projected variance was 1.92 times higher than the variance in the dataset. Additionally, it was determined that a substance that had showed a spectrum of good signal strength could still be classified correctly when measured through various containers, such as glass vials, Petri dishes and a white paper envelope. A qualitative comparison with a microNIR spectrometer (908.1-1676.2nm) showed a similar spectrum to the SciO in their shared wavelength. Two samples showed a spectrum of higher quality when measured with the microNIR than when measured with the SciO. For substances with a good signal strength in the short-wave NIR spectrum, it was possible to obtain a robust classification using the SciO spectrometer.</p>

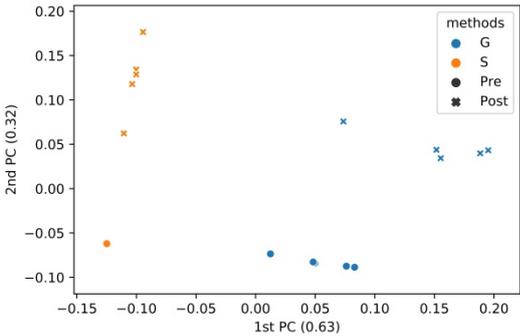
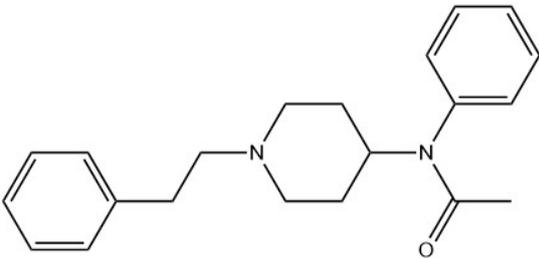
<b>Student</b>	<b>Sofie Huisman</b>
<i>Research carried out at</i>	University of Lausanne
<i>Supervisor</i>	prof.dr. Natalie Kummer
<i>Title thesis</i>	Optimisation of a non-targeted HPLC-HR-QToF-MS/MS method for the analysis of forensic samples of new psychoactive substances
<i>Abstract</i>	<p>Wastewater based epidemiology using LC-MS/MS has become a common and successful tool for the targeted monitoring of illicit drugs throughout the world. With its high sensitivity it has been able to identify and quantify drugs at concentrations as low as 0.2 pg/ml. However, compounds that are not selected for analysis stay undetected in wastewater and a full picture of all the drugs being (ab)used is not given. This approach, therefore, fails in the real time detection of non targeted drugs that have entered the market in any given region. In this study, a novel UPLC-IMS-QTOF-MSE system with non-targeted screening has been investigated for the analysis of illicit drugs in wastewater. It was validated based on limits of detection and quantification, linearity, accuracy and precision. The limits of detection for cocaine, benzoylecgonine and MDPV were as low as 0.1 to 2 pg/ml and the limits of quantification were 10 pg/ml. For amphetamine, methamphetamine, MDMA, MDA, MDEA, mephedrone and methedrone the limits of detection were between 0.1 and 1 ng/ml. The limits of quantification were between 1 and 20 ng/ml. The linearity for most compounds had an <math>R^2 &gt; 0.99</math>, the exceptions were amphetamine and methedrone. Within-run and between-run precision was found to be within the acceptable RSD <math>\pm 15\%</math> but the accuracy was unacceptable (greater than <math>\pm 15\%</math> error). Preliminary matrix effect evaluation showed large variations between the compounds. Finally, 24 wastewater samples from St. Gallen, Geneva and Bern were analysed and cocaine, benzoylecgonine, methadone, EDDP, MDMA and 6-MAM were detected. Reprocessing of the data was then performed using a larger database including 730 NPS compounds and pharmaceutical drugs. Various pharmaceuticals could be identified as well as cocaethylene and caffeine. The screening platform UNIFI identified candidate masses for the peaks that did not correspond to any compound in the database, and chemical formulae could be elucidated and run through databases (such as ChemSpider). Through the database searches, it was possible to determine a potential compound (stercobilin) for one of the investigated candidate masses.</p>

<b>Student</b>	<b>Alica Kandler</b>
<i>Research carried out at</i>	Institute of Environmental Science and Research (ESR) New Zealand
<i>Supervisor</i>	Gerhard Wevers
<i>Title thesis</i>	Crowbar Paint Projec
<i>Abstract</i>	<p>Indistinguishable paint samples from burglary cases are a common sight in forensic laboratories in New Zealand. Often, due to the absence of population study data, the evaluation of the evidential values is performed rather subjectively. The focus of this paper was to create a database of crowbar and scene paint traces, determining the occurrence of paint characteristics as color and chemical composition in the population, and consequently provide examiners with valuable data to help calculate a more accurate and objective likelihood ratio (LR). Results from a performed transfer simulation experiment showed, that cross-transfer can be expected to occur in 100% of the cases, emphasizing the availability of paint evidence in burglary cases. Moreover, the collected data of 64 crowbar paint and 376 transferred scene paint samples, underlined the high dependence of the calculated LR on characteristics such as color and chemical composition, by returning LRs of 68 and almost 10,000 for rather common and rather rare indistinguishable paint samples, respectively. Additionally, a discrimination rate of just over 98% for the crowbar paint samples, based on visual and microscopical examinations as well as Fourier Transform Infrared Spectroscopy, emphasized the low probability of finding two indistinguishable paint samples of different origins. These results further outline the possible future potential of crowbar paint evidence, given the implementation of a more conscious and frequent collection process. Overall, the importance of using population study data for the assessment of evidential values was pointed out to maintain a high quality in the future work of forensic scientists. Furthermore, multiple new research ideas were presented based on the collected findings, of which the implementation of a crime mapping database, to track the usage of the same tool at different crime scenes, seemed the most interesting and promising.</p>

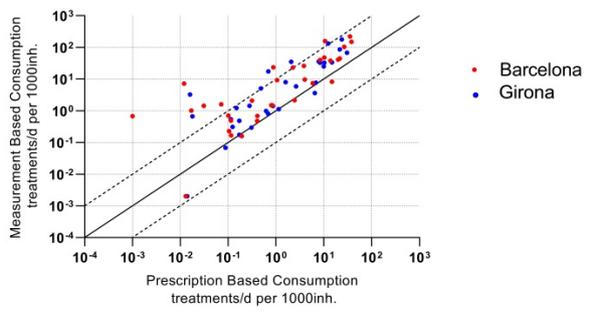
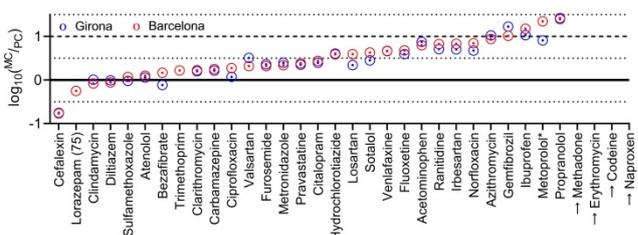


<b>Student</b>	<b>Frederike Oetker</b>
<i>Research carried out at</i>	UvA
<i>Supervisor</i>	Annemieke Hulsbergen
<i>Title thesis</i>	Assessment of risk and injury potential during ATM bombings
<i>Abstract</i>	<p>This paper answers the question what the injury and damage potential of ATM bombings is. Using flash powder (FP) and ammonium nitrate (AN) as the primary ingredients for the explosive charge, eight ATMs were exploded and the effects were analysed. Five ATMs were exploded by inserting the FP explosive charge in a metal casing through the money slot into the ATM vault. The other three ATMs were exploded by inserting one plastic and tape wrapped AN charge inside of the ATM and applying another plastic and tape wrapped AN charge to the outside of the ATM. Using pressure meters, the shockwave of the explosions could be recorded. For the three ATMs with the charge applied both inside and outside, the lung damage potential via the shockwave was categorized as 99% or higher in the initial meters, while the other five ATMs had a shockwave with a significantly lower damage potential. The permanent ear damage potential behaves accordingly with thresholds between 0 and 30 meter. Similarly, the lethality due to penetrative and blunt trauma of the shrapnel pieces is higher with a larger amount of charge, and with a charge applied to the outside of the ATM. A higher density of shrapnel and debris pieces was recorded with increased amounts of charges applied to the inside and outside of the ATM. The penetrative shrapnel possesses the highest lethality potentials across all experiments with a range up to more than 50 meter, with the blunt trauma lethality up to the same range but in lower percentages. In conclusion, the lethality is increased with the application of charge to the outside of the ATM, due to the undamped shockwave and the higher velocity of shrapnel and debris.</p>

Student	Roos Hessels
<i>Research carried out at</i>	NFI
<i>Supervisor</i>	Karlijn Bezemer MSc
<i>Title thesis</i>	ETN IRMS Project
<p data-bbox="183 441 287 474"><i>Abstract</i></p> <div data-bbox="199 548 758 750" style="text-align: center;"> <p data-bbox="199 750 438 761"><i>Mixed acid and nitrate salt route for ETN synthesis.</i></p> </div> <div data-bbox="191 840 758 1120" style="text-align: center;"> <p data-bbox="191 1131 351 1153"><i>Various erythritol sources</i></p> </div>	<p data-bbox="794 441 1414 1921">In this research isotope ratio mass spectrometry (IRMS) was used to differentiate the home-made explosive erythritol tetranitrate (ETN) and its erythritol and nitrate precursors to contribute to chemical attribution in forensic explosive investigations. Attribution information on precursors and produced explosives can give valuable information, i.e., linking precursor material in a suspect's house to an explosive that is found on a crime scene. ETN is a strong explosive which is gaining popularity among criminals and terrorists. The possible threat that ETN forms makes it forensically relevant to investigate. Different erythritol and nitrate precursors were collected, and carbon, hydrogen, oxygen and nitrogen isotope values were measured to get an estimation on the degree of variation and differentiation within the precursor materials. A selection of precursors was used to prepare ETN samples following two synthesis routes, the so-called mixed acid and nitrate salt route. These synthesis routes are most commonly encountered in a forensic context. A strong correlation was found between the carbon isotope values of erythritol and produced ETN, which allows direct linkage between precursor and corresponding ETN-end product. Unfortunately, the relative small range of carbon isotope values in the erythritol precursors limits its differentiation potential. For the nitrate precursors and produced ETN-end a strong correlation was observed for the nitrogen isotope values, the different nitrate sources showed a wide range in nitrogen isotope values, making it possible within the selected samples, to link a number of nitrate precursors to the produced ETN-end products, and also made it easier to differentiate between the used precursors. Although it is possible to link ETN precursors to ETN end-products, it is difficult to put evidential value to the specific links. To connect evidential value, more information is needed on how unique and distinctive the link is. However, information obtained in this project can forensically still be very valuable, for example the possibility of excluding a certain precursor as the donor of the produced ETN.</p>

Student	Djarah Kleiweg
<i>Research carried out at</i>	TNO
<i>Supervisor</i>	dr. Daan Noort
<i>Title thesis</i>	Chemical profiling of fentanyl in complex matrices
<p data-bbox="177 430 288 461"><i>Abstract</i></p>  <p data-bbox="188 909 695 1010">PCA plot of the GC-FID measurements separating synthesis method G and S with before and after metabolism samples</p>  <p data-bbox="188 1384 440 1415">Structure of fentanyl</p>	<p data-bbox="788 430 1417 1601">Chemical profiling has been used in forensic investigations to determine whether two compounds share a common origin, synthesis method or manufacturer. In the field of illicit drugs, this is usually done by characterizing the impurity profile of a seized sample, followed by comparison to a database or other seized samples. Current literature focuses on the analysis of bulk samples, however extending impurity profiling to biomedical samples would open up new possibilities in the forensic investigation. In the present study, human liver microsomes were used to determine the effect of human metabolism on the impurity profile of fentanyl. Two synthesis methods (Siegfried and One-Pot) were used to synthesise fentanyl, after which the impurity profiles of the samples were constructed with GC-MS, GC-FID, LC-Q-TOF-MS and LC-Orbitrap-MS. Statistical analysis with principal component analysis (PCA) identified acetylfentanyl as the most important marker compound to discriminate between the two synthesis methods. While acetylfentanyl itself is not stable during metabolism, its discriminating role can be taken over in post-metabolism samples by its metabolite acetylnorfentanyl. Six other marker compounds were identified that can discriminate between the two synthesis methods, and that were stable during metabolism. To apply the results in a forensic framework, linear discriminant analysis (LDA) was used to calculate likelihoods ratios (LRs). It was found that the separation of the two synthesis methods was large enough to result in extremely high LRs. The present work demonstrates a first step towards inclusion of biomedical samples in the field of chemical profiling.</p>

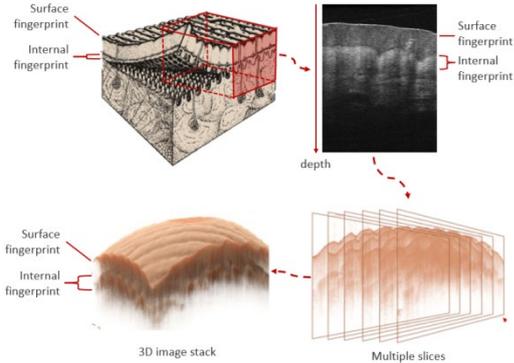
Student	Nicole Schröter
<i>Research carried out at</i>	Catalan Institute for Water Research
<i>Supervisor</i>	mr. Pablo Gago-Ferrero
<i>Title thesis</i>	Socio-economic changes in wastewater: licit and illicit drug use patterns in Barcelona and Lleida
<i>Abstract</i>	<p>Wastewater-based epidemiology can estimate the behaviour of a large-scale population regarding the consumption of specific substances based on chemical analysis of wastewater. In the present study, the consumption of a wide range of licit and illicit drugs was back-calculated following these methodologies in two cities of the Northeast of Spain. Then, these data was compared with the one obtained from official prescription data provided by health authorities. The wastewater was analyzed using solid phase extraction coupled to tandem mass spectrometry (SPE-LC-MS/MS) and prescription data mining was accomplished via database inquiries with standard query language (SQL). A detailed comparison for each group of drugs between these complementary methods was obtained. This constitutes valuable information to improve and validate the wastewater-based approach considering the different potential uncertainties (e.g. excretion rate or daily dosage). Overall, the consumption of (il)licit drugs in both investigated cities was similar. Consumption based on chemical measurements showed generally higher compared to the official prescriptions. Particular large deviations were observed for certain compounds (e.g. most analgesics) since there is a high non-prescription consumption. However, significant differences were also observed for highly prescribed drugs (e.g Gembrofizil, Pravastatine, Lorazepam, Lorsartan, Irbesartan, Hydrochlorotiazide, Venlafaxine, Azithromycin). Poor accuracy in excretion rates and daily doses was found to be major uncertainties regarding estimation of consumption from wastewater data. Ultimately, correlation analysis showed that the use of prescription data is a useful strategy to validate and quantify the magnitude of uncertainty of back-estimations in drug consumption using wastewater-based epidemiology.</p>



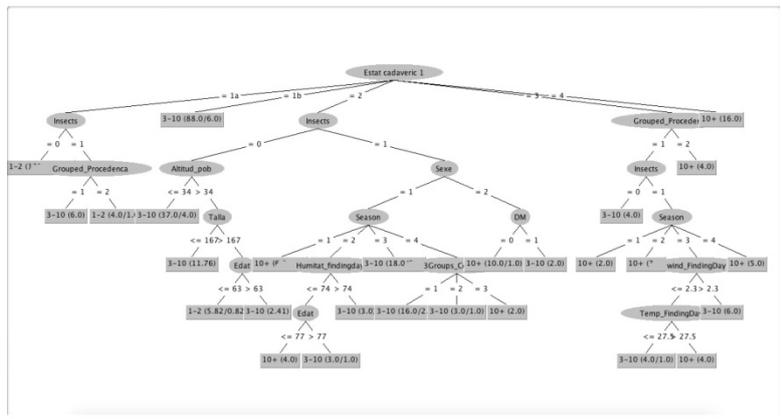
## Forensic Medicine

<b>Student</b>	<b>Heleen Coreelman</b>
<i>Research carried out at</i>	Gent University
<i>Supervisor</i>	prof.dr. Koenraad Verstraete
<i>Title thesis</i>	Multi-factorial forensic age estimation: Combining radiographs of the third molars, the left wrist and both clavicles
<i>Abstract</i>	<p>Background - Forensic age estimation in living adolescents and young adults can be important in civil procedures, criminal investigations, asylum cases and sports. To acquire data for forensic age estimation in living persons, medical imaging is the current gold standard. Nevertheless, no internationally accepted standardised age estimation procedure exists, thereby causing disparities between results from different centres. Considering adolescents and young adults, the interdisciplinary Study Group on Forensic Age Diagnostics (AGFAD) recommends that forensic age estimation in the living should combine (1) a physical examination including anthropometric data, sexual maturity characteristics and medical history, (2) a conventional radiography (CR) examination of the left hand, and (3) a dental examination with a panoramic radiograph. If the hand bones reached full maturation, an additional CR or computed tomography (CT) examination of the clavicles is suggested. In Belgium and the Netherlands, only clavicle CR is applied, while clavicle CT is actually recommended. Aim - Two-dimensional and three-dimensional imaging of the left wrist and both clavicles were compared for forensic age estimation. Material &amp; Methods – CR and magnetic resonance imaging (MRI) were prospectively conducted of 108 healthy Caucasian volunteers (52 males, 56 females) with ages ranging from 16 and 21 years. MRI was chosen as an alternative to CT, because conducting CT in a prospective study with healthy volunteers would not be ethically justifiable. Skeletal development was assessed by allocating stages and/or atlas standards to the distal radius and ulna, and the sternal ends of both clavicles. For clavicle CR, one posteroanterior and two oblique radiographs were assessed simultaneously. Inter-observer agreements were quantified, and descriptive statistics on age distributions were reported. Results - Inter-observer agreements for both wrist CR and MRI were similar, as were those for staging techniques and atlas methods. Conversely, inter-observer agreements for clavicle CR were lower than those for clavicle MRI. Furthermore, wrist CR and MRI age distributions were similar, as were the age distributions between the staging techniques and atlas methods. Conversely, the possibility to apply (profound) substages to clavicle MRI provided a more gradual increase in the age distributions with increasing stages, compared to clavicle CR. Conclusion - For multi-factorial age estimation based on the left wrist and both clavicles, two-dimensional imaging seems to suffice for the wrist, while three-dimensional imaging seems necessary for the clavicles. Furthermore, although less straightforward, a hand/wrist atlas method appears to be equally useful as a wrist staging technique for forensic age estimation.</p>

<b>Student</b>	<b>Nina Eckhardt</b>
<i>Research carried out at</i>	NFI
<i>Supervisor</i>	dr. Nicole van Woerden
<i>Title thesis</i>	Evaluating the value and role of (preliminary) DECCA advice in physical child abuse assessment by the Netherlands Forensic Institute
<i>Abstract</i>	<p>The Dutch Expertise Centre for Child Abuse (DECCA) is an organization founded in December 2014 that aims to provide health professionals with quick and reliable advice on suspected physical child abuse. While their value from the viewpoint of health professionals has been investigated, this study focused on the continuation and implementation of their advice in cases referred to the Netherlands Forensic Institute (NFI). Medicolegal reports from the NFI (n=172) and corresponding DECCA advisory reports (n=56) from 2015-2019 were reviewed, applying descriptive statistics and logistic regression analyses to compare their Bayesian conclusions, study the adherence to their advice, and detect trends in the requesting of DECCA advice. On average, 13% of advised examinations had not been performed, and no significant predictive model for the presence of an advisory report was found. Additionally, 15 and 33 comparisons of the Bayesian conclusions made by DECCA and the NFI showed that over 90% of their conclusions were the same or differed one step on the verbal likelihood scale. However, potential incorrectness and unclear documentation of DECCA Bayesian conclusions makes the validity of these comparisons questionable. This study has presented various indications of an adequately functioning DECCA when it comes to (the requesting of) their advice and their conclusions. However, the use of Bayesian reasoning and the implementation of their goal for presenting quick, reliable, and understandable conclusions on suspected physical child abuse requires thoughtful reconsideration.</p>

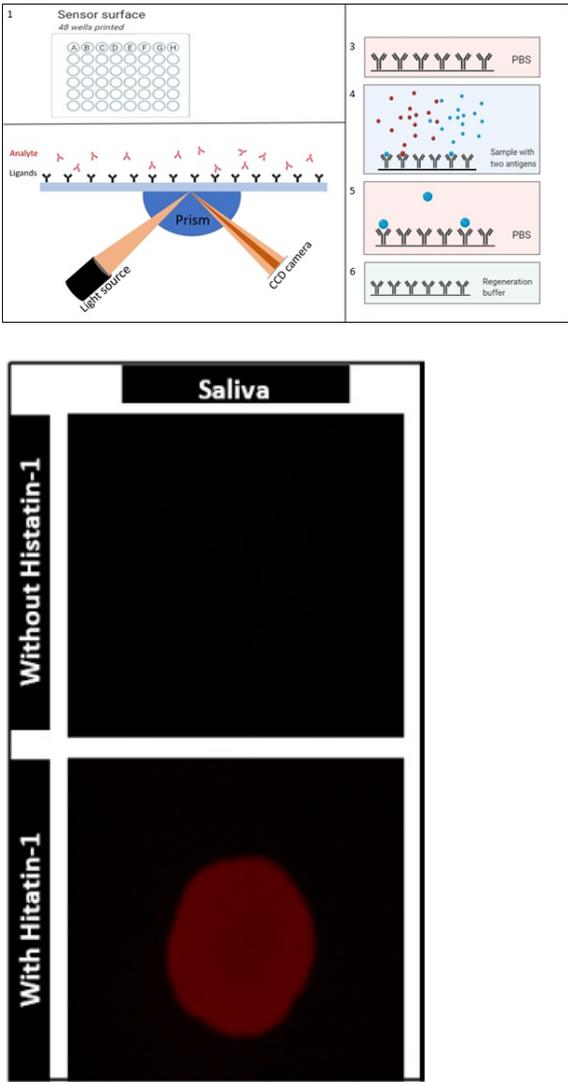
<b>Student</b>	<b>Lisa Klok</b>
<i>Research carried out at</i>	Amsterdam UMC
<i>Supervisor</i>	Leah Wilk MSc
<b>Title thesis</b>	Extraction of Surface and Internal Fingerprints from Optical Coherence Tomography Scans for Forensic Identification
<p><b>Abstract</b></p>  <p>Illustration of the skin and how the images obtained by OCT are used for a 3D representation. The skin (bottom right), and different structures within the tissue, is captured in multiple B-scans. Stacking of these B-scans leads to a 3D representation of the skin.</p>	<p>Fingerprints are one of the best known and well-established physiological traits used for personal identification and verification. They are commonly used as a biometric in our private life and by a multitude of governmental organizations. Optical coherence tomography (OCT) is increasingly proposed as an alternative fingerprint acquisition system that is robust and resistant to spoof attacks. OCT is able to capture the inner structures of the finger. The inner layers have a similar topology to the fingertip's surface and can be used to extract internal fingerprint images. The internal fingerprint is unaffected by superficial defects such as scars and wrinkles and can aid in robust fingerprint verification and identification. All published work focuses on fingerprint identification in the living. However, the feasibility of OCT for postmortem fingerprinting has never been researched. Fingerprint identification is essential to establish the identity of the deceased in both medicolegal investigations and mass fatalities after disasters. It is still unknown how decomposition processes will affect the OCT scans and whether surface and internal fingerprints can still be extracted. In this study, algorithms are developed for the extraction of surface and internal fingerprints from OCT scans performed in a touchless as well as a touch-based manner in the living. The developed algorithms are able to extract surface and internal fingerprints from the living from touch-based and touchless OCT scans. The fingerprint images can be successfully used in fingerprint matching software for verification and identification purposes. Additionally, the possible use of OCT for postmortem fingerprinting is explored. Two fingertips of a deceased human body that was buried for a duration of ten months are examined to determine the effects of decomposition on the acquired images. The OCT scans of the deceased show changes in the backscatter profile in the fingertip, which is indicative of structural changes in the layer composition of the skin. This research shows that developed methods for fingerprint identification with OCT in the living cannot be directly translated for postmortem use. However, with minor adjustments of the developed algorithm, fingerprints are still extracted from the touch-based OCT scan of the deceased.</p>

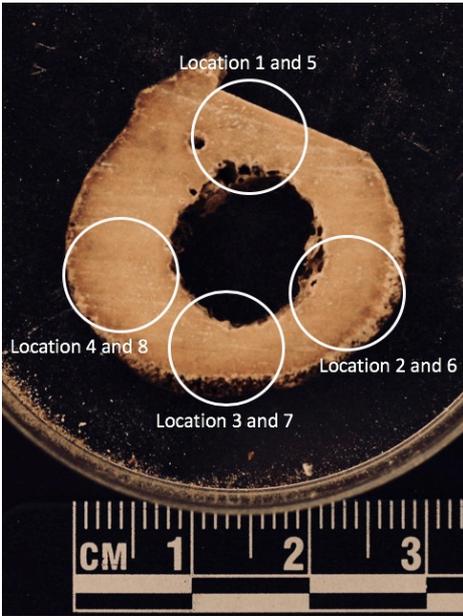
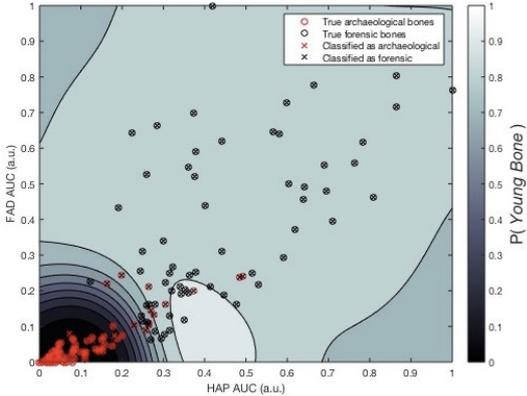
<b>Student</b>	<b>Karin Körsegaard</b>
<i>Research carried out at</i>	Universitat Autònoma de Barcelona
<i>Supervisor</i>	prof.dr. Ignasi Galtés
<i>Title thesis</i>	Forensic and epidemiological analysis of decomposed bodies in Catalonia
<i>Abstract</i>	<p>After death human body is subject to the processes of autolysis and putrefaction. Notably, the changes in cadaver during decomposition complicate its identification and the perception of the cause and manner of death, as well as the estimation of the post-mortem interval (PMI). The process and rate of decomposition is impacted by various intrinsic and extrinsic factors that vary across countries and regions. The influence of several factors and the process of decomposition were studied for the first time in the province of Barcelona in Catalonia, Spain. This research concluded that the most significant factors affecting the process and rate of decomposition in the province of Barcelona are age, the pre-existing medical conditions of diabetes or neoplasia, cause of death, outside temperature and season. Considering the various variables studied in this research, a predictive model was developed as a probabilistic approach to estimate the PMI with an accuracy of 82.1%. This is a preliminary model still and needs some improvements in the future, yet, it is a novel approach and allows the forensic doctors to predict how many days the subject has been dead for.</p>



A decision tree using the J48 algorithm to estimate the PMI taking into account some intrinsic and extrinsic variables. Variables considered: insect succession, decomposition phase (Estat cadaveric 1), season, gender (Sexe), age (Edat), spot of discovery (Grouped\_Procedencia), region (Groups\_Comarca), height of the subject (Talla), altitude, temperature, wind speed and humidity on the finding day, diabetes (DM).

Overview of the correlation of prescription and measurement based consumption of licit drugs for Barcelona and Girona. Solid line = consumption of prescription and measurement estimated data are the same; dotted line = one magnitude (10) difference.

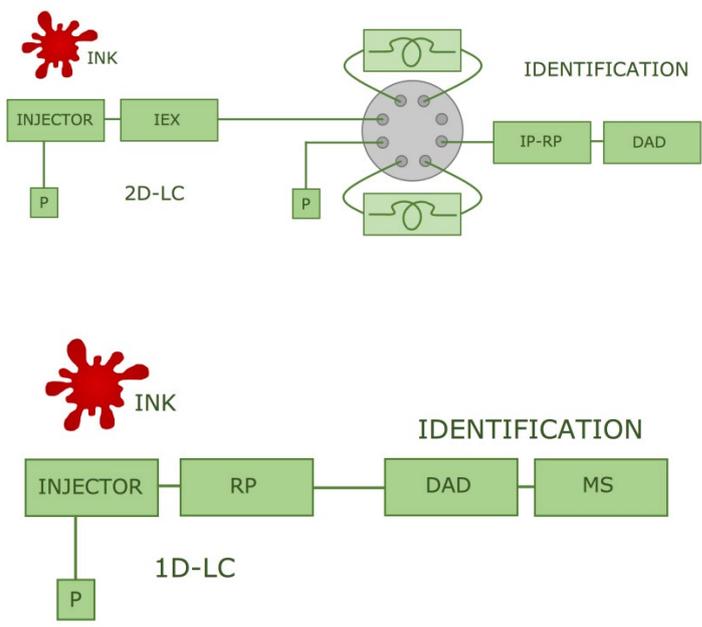
<b>Student</b>	<b>Lisanne Limburg</b>
<i>Research carried out at</i>	Amsterdam UMC
<i>Supervisor</i>	dr. Nihad Achetib
<i>Title thesis</i>	Using Surface Plasmon Resonance to determine the age of deposited body fluids
<i>Abstract</i>	
<p><b>Abstract</b></p> 	<p>Identifying biological samples found on crime scenes is of major importance in forensic practices. On-site BFI tests are often not sensitive and specific enough to robustly identify body fluids. A new method for body fluid identification has recently been introduced: surface plasmon resonance imaging. Antibodies against body fluid specific proteins are printed on the SPR sensor, enabling the identification of body fluids present in the sample. Previous research shows that body fluids can be identified using clustering analysis; however the method shows some limitations. Using PCA prediction scores five out of eight unknown samples were identified; with three samples remaining inconclusive. This study aimed to improve the body fluid identification method, by testing four different improvements. Firstly, a new biomarker Histatin-1 was tested for the identification of saliva. Secondly, additional kinetic parameters present in surface plasmon resonance data, Rmax and initial slopes, were tested for their use in body fluid identification. Furthermore, forensic samples are often complex matrices of multiple proteins in unknown concentrations, therefore a concentration determination experiment was performed to construct calibration curves. Lastly, curves of each body fluid were classified and a manual was created for presumptive body fluid identification. Results showed that Histatin-1 was specific for saliva alone and could be detected in dilutions up to 1:100. Therefore it can be added to the body fluid identification method. Additional kinetic parameters did not show promising results and could not be used for body fluid identification based on clustering analysis. Concentration determination was only successful using the biomarker ICAM5, making it possible to construct calibration curves, body fluid specific markers did not yield results. Lastly, curve classifications showed that body fluids could be distinguished from each other based on association and regeneration curve shapes. In summary, two improvements were made: adding a new biomarker for the identification of saliva and making presumptive identification of bod fluids possible based on curve shapes.</p>

<p><b>Student</b></p>	<p><b>Daphne Muijderman</b></p>
<p><i>Research carried out at</i></p>	<p>Amsterdam UMC</p>
<p><i>Supervisor</i></p>	<p>prof. dr. Maurice Aalders</p>
<p><i>Title thesis</i></p>	<p>Determining the age of bones with fluorescence spectroscopy</p>
<p><b>Abstract</b></p>  <p>The locations on the bone sample that were measured.</p>  <p>A support vector machine model based on the compounds HAP and FAD.</p>	<p>When bones are found it is important to know whether the bones are forensically relevant or archaeological material. This distinction is based on the age of the bones in a way that bones that date from before 1920 are archaeological material and bones that date from after 1920 are considered to be forensic. Since 1920 there is a missing person's database in the Netherlands and the donor of the bones could be traced back when the bones are dating from after 1920. The current method of dating bones is radiocarbon dating. This is a time-consuming method, creating the need for a faster method to make it possible for investigators to know immediately how to treat bones when they are found. In this research, the feasibility of a method based on fluorescence spectroscopy is investigated. The compounds collagen, hydroxyapatite (HAP) and flavin adenine dinucleotide (FAD) are present in the bone tissue and they are expected to decline after death due to the decomposition of bone. The differences in amounts can be measured with fluorescence spectroscopy. Bones from five different time periods, ranging from 1500 to 2003, are used in this research. Several models were designed to determine the age of bones: ratios of collagen, HAP and FAD, k-means clustering analysis, principal component analysis (PCA), linear discriminant analysis (LDA) and support vector machine (SVM) models. The HAP-FAD ratio showed a clear decrease over time, but due to the large amount of variation within the time periods this model could not be used in determining the age of bones. The other models were used to create a distinction between the archaeological and forensic bones, in which the SVM models proved to be the most promising method to apply in practice. One of the models resulted in a sensitivity of 86.764% to 100% and a specificity of 73.26% to 87.65%. However, many improvements need to be achieved before this model could be used by the police and crime scene investigators and before it could replace the method of radiocarbon dating. Overall, SVM has the potential to become an additional method to distinguish between archaeological and forensic bones, leading to less bone samples that need to be investigated by using radiocarbon dating.</p>

<b>Student</b>	<b>Jacky Haring</b>
<i>Research carried out at</i>	VU University
<i>Supervisor</i>	dr. Carlos Martín Alberca
<i>Title thesis</i>	Age estimation of human biological traces - Identifying important chemical biomarkers
<i>Abstract</i>	<p>Over the years, examining activity level propositions has gained importance in forensic investigations. These analyses can add significant value to forensic evidence by allowing law enforcement to distinguish between crime-related and unrelated traces. Age estimation of body fluids is an example of such research. Recently, an ageing method was proposed (Van Dam et al., 2014) that uses a change in fluorescent emission signals of fingermarks to estimate the time since deposition. However, the exact origin and mechanism behind the fluorescence observed to appear in the visible range of the spectrum remains unclear. A better chemical understanding of these phenomena can improve such ageing methods. This study has used fluorescence spectroscopy to investigate the visible fluorescence, which has also been called deep-blue autofluorescence (Niyangoda et al., 2017) and FOX fluorescence (Van Dam et al., 2014), in fingermark residue components. Visible fluorescence is believed to arise due to interactions between carbonyl groups and nitrogen atoms. A sufficient level of abundance and rigidity of molecules allows extended electron delocalisation, which results in structures that are (more) readily excited (Chen et al., 2018). Results presented in this work show that unoxidized individual proteins (human serum albumin and lysozyme), amino acids (glycine, <math>\beta</math>-alanine, proline and tryptophan) and lipidic components (squalene, cholesterol, several fatty acids and a wax ester) produce fluorescence in the visible part of the spectrum. All compounds (except for proline and tryptophan) were individually analysed by MALDI-MS and could be detected. Furthermore, a model system composed of an eccrine and sebaceous component, representing fingermark residue, was investigated. Aromatic and visible fluorescence was detected at <math>t = 0</math> in both the model system and its eccrine component. It was shown that an observed decrease in aromatic fluorescence of the eccrine component, containing solely proteins (HSA and lysozyme) and amino acids (glycine and alanine), was not accompanied by modifications of these compounds (analysed by MALDI-MS). However, the exploratory MALDI-MS study of the model system indicates that chemical interactions may occur. It is hypothesized that the sebaceous component (containing lipidic molecules) plays an important role. To conclude, this study demonstrates possible origins of visible fluorescence in fingermark residue and uses different mechanisms proposed in literature to discuss the observed changes in model systems. The findings can be used in future research to further optimize a model system suitable for both fluorescence and mass spectrometric analyses.</p>

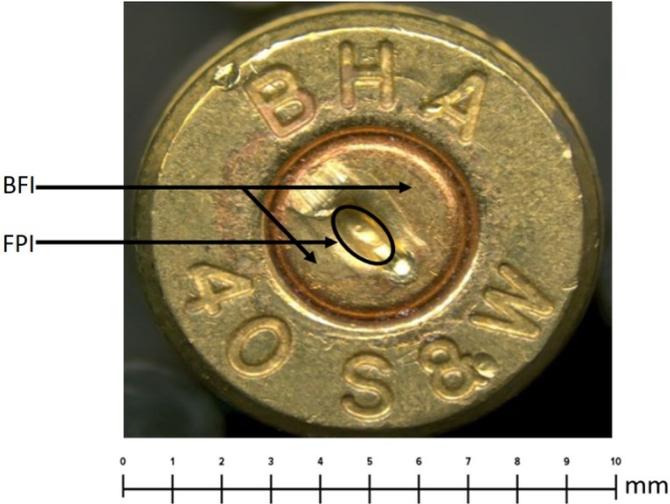
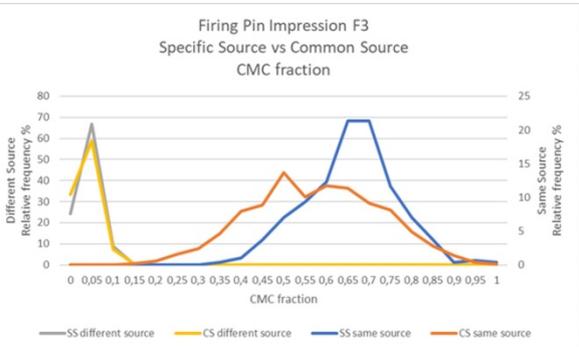
Student	Annabelle Kuipers																		
Research carried out at	NFI																		
Supervisor	dr. Wouter Karst																		
Title thesis	What is the value of the physical investigation that is done in child sexual abuse cases?																		
<p data-bbox="177 472 288 506"><b>Abstract</b></p>  <p data-bbox="177 808 628 842">a forensic collection kit © Bert Beelen</p> <div data-bbox="193 913 751 1332"> <table border="1"> <caption>Data from pie charts: Agreement between positive sampling locations and history of events</caption> <thead> <tr> <th>Victim Group</th> <th>Category</th> <th>Does not match history of events</th> <th>Matches history of events</th> </tr> </thead> <tbody> <tr> <td rowspan="2">Prepubertal victims</td> <td>location of sperm(fluid)</td> <td>8%</td> <td>92%</td> </tr> <tr> <td>location of non-self DNA</td> <td>1%</td> <td>97%</td> </tr> <tr> <td rowspan="2">Pubertal victims</td> <td>location of sperm(fluid)</td> <td>19%</td> <td>81%</td> </tr> <tr> <td>location of non-self DNA</td> <td>7%</td> <td>88%</td> </tr> </tbody> </table> </div> <p data-bbox="177 1352 684 1458">Graph showing the agreement between positive sampling locations and the given history of events.</p>	Victim Group	Category	Does not match history of events	Matches history of events	Prepubertal victims	location of sperm(fluid)	8%	92%	location of non-self DNA	1%	97%	Pubertal victims	location of sperm(fluid)	19%	81%	location of non-self DNA	7%	88%	<p data-bbox="767 472 1417 506"><b>OBJECTIVE:</b> To further improve the acute forensic medical examination and forensic evidence collection in acute child sexual abuse cases, this study aims to give an overview of the child sexual abuse cases investigated by the Netherlands Forensic Institute and investigate which factors are associated with successful forensic evidence collection. <b>METHODS:</b> data from 355 acute medical examinations conducted by the Netherlands Forensic Institute was collected prospectively from August 2016 until August 2019. This data was combined with the DNA results from the corresponding forensic evidence collection kits. Statistical analysis was done using bivariable and multivariable linear logistic regression, resulting in ORs and adjusted ORs. <b>RESULTS:</b> 40% of all evidence collection kits was send in for analysis. 52 out of those 128 kits (40.6%) were positive for non-self DNA and 51% of the kits taken within 24 hours were positive for non-self DNA. Of all analysed kits, 31% yielded a match with a suspect in either the evidence collection kit or on the clothes. Pubertal victims had a higher percentage of positive kits compared to prepubertal victims. Bathing after the incident decreased the percentage of positive kits from 62% to 38%. Bathing was negatively associated with detecting superficial non-self DNA. In 12% of cases involving pubertal victims, there was a disagreement between a positive sampling location and history of events; 7% of cases included non-self DNA and 5% suspect DNA on non-disclosed locations. Most tested demographic and clinical factors showed no association with detection of forensic evidence. An increase in days between incident and examination was however found to be negatively associated with finding suspect DNA in pubertal victims. <b>CONCLUSIONS:</b> for forensic evidence collection, timely examination seems to be an important factor for a positive forensic evidence collection kit, as well as not having bathed and a child being pubertal. The agreement between the location of forensic evidence and history of events was found to be poor. This study therefore underlines the importance of not using a targeted evidence collection strategy based upon disclosure for sampling in child sexual abuse cases.</p>
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## Forensic Physics and Forensic Chemistry

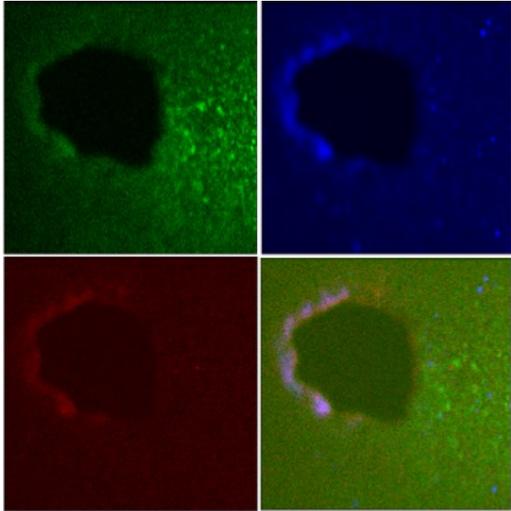
Student	Alissa Sczyslo
Research carried out at	UvA
Supervisor	dr. Bob Pirok
Title thesis	LC-MS analysis of IBNS inks on euro currency
<p data-bbox="183 533 287 560"><i>Abstract</i></p> 	<p data-bbox="930 533 1404 1176">As ATM raids are still a high risk for banks, the security measure of staining banknotes with Intelligent Banknote Neutralization System (IBNS) inks has been introduced. In order to distinguish those inks from commercially non-crime related inks and dyes, an analytical method was developed based on two-dimensional liquid chromatography coupled to a diode array detector (2DLC-DAD) and liquid chromatography coupled to DAD and a mass spectrometer (LC-DAD-MS). The methods were applied to analyze the compounds of the IBNS inks used in the Netherlands. Possible specific markers of the security inks were compared to commercially available different types of ink.</p>

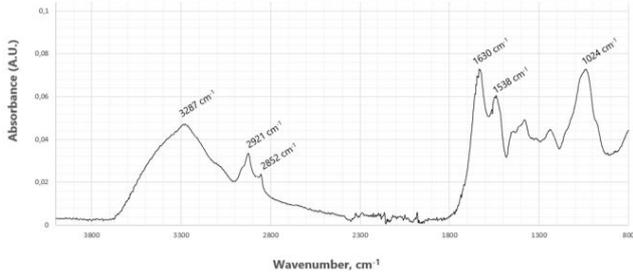
## Forensic Statistics

<b>Student</b>	<b>Jorit Delen</b>
<i>Research carried out at</i>	NFI
<i>Supervisor</i>	dr. Martin Baiker-Sorenson
<i>Title thesis</i>	Forensic Evaluation of Objective Methods for Automated Analysis of Glock Cartridge Case Marks
<i>Abstract</i>	<p>In the current system of firearm examination, when comparing a questioned bullet or cartridge case with a reference often the examiner has to make several subjective calls during the process. There have been several calls for a better statistical foundation for current methods of firearm examination, and the move towards more automatic systems which will be less subjective. In this study, we will use one of those new automatic systems, a program named Scratch, that provides similarity scores of comparisons based on Areal Cross Correlation Function (ACCF) and Congruent Matching Cells (CMCs). We use this program to analyze the individuality and repeatability of firing pin impressions and breech face impressions that are left on cartridge cases by Glock firearms. To do this, we took a set of 200 Glock firearms of type 17, 19 and 26, and fired each 4 times for a set of 800 cartridge cases. A cast of these cases was made, and these cast were scanned in with 3d scanning equipment. The 3d data can be compared to create Known Match and Known Non Match distributions for both the ACCF and CMC fraction. The primer material could also be an issue, so each firearm was shot twice with Fiocchi-branded cartridge cases which had a nickel primer (which is softer), and Sellier \&amp; Bellot-branded cartridge cases which had a brass primer (which is harder). For the breech face impressions, it was found that a part of the S\&amp;B ammunition had a dot-like pattern on the primer which massively influenced the comparison scores. These were filtered out. For both mark types and similarity measures, the results seemed reasonably good, however firing pin impressions performed better than breech face impressions on both ACCF and CMC fractions. For firing pin impressions, it was found that softer materials provided better results for both the ACCF scores and CMC fractions. For breech face impressions, it was found that it was more important that both cartridge cases had the same primer material, then what that material was.</p>

<p><b>Student</b></p>	<p><b>Jeroen Letteboer</b></p>
<p><i>Research carried out at</i></p>	<p>NFI</p>
<p><i>Supervisor</i></p>	<p>dr. Martin Baiker-Sorenson</p>
<p><i>Title thesis</i></p>	<p>Common Source versus Specific Source approach for automated comparison of Glock cartridge case marks</p>
<p><i>Abstract</i></p>  	<p>Firearms are often used in crimes. The comparison of marks on cartridge cases can then play an important role in the forensic investigation. Depending on the situation a Specific Source (SS) or Common Source (CS) approach can be used to determine the strength of the evidence. Since the CS approach takes less time, it is of interest to know whether it can be used for situations that in theory would require a SS approach. Therefore the following research questions are studied in this report: 'Is there a significant difference between Common Source and Specific Source distributions for firing pin impressions on Glock cartridge cases?' and 'Is there a significant difference between Common Source and Specific Source distributions for breech face impressions on Glock cartridge cases?'. For this study 20 Glock pistols were used and with each pistol 25 test shots with Fioocchi 9mm Luger cartridges were fired. A 3D measurement system was used to scan the cartridge cases. The software Scratch was used to crop the firing pin and breech face impression from each scan. Similarity scores between the different cartridge cases were calculated in order to build SS and CS distributions for all 20 firearms. Statistical tests were performed to find out if there is a significant difference in the distributions for both mark types. The results showed that for a substantial part of the firearms the SS and CS distributions are significantly different for both the firing pin impressions as well as for the breech face impressions on Glock cartridge cases. Therefore it is concluded that it is unjustified to use the CS approach for a specific source situation, since the difference in the distributions could lead to a difference in the evidential strength.</p>

## Other

<b>Student</b>	<b>Luca Cannatella</b>
<i>Research carried out at</i>	Rijksmuseum
<i>Supervisor</i>	dr. Katrien Keune
<i>Title thesis</i>	Validating the Authenticity of 17th Century Royal Clothing with the Use of Forensic Techniques
<i>Abstract</i>	<p>This research uses the forensic methodology to help authenticate 17th century war relics, currently held by the Rijksmuseum, that were supposedly connected to the deaths of two father and son noblemen, Ernst and Hendrik Casimir. The research uncovered traces of gunshot residue, using both SEM-EDX and 2D-mXRF, going a long way to proving the items were damaged by gunshots in the past and authenticating the relics. Other pathways of investigation were using XRF to confirm if stains were in fact blood on multiple items and forensic anthropology which found that bones in the collection did not align with the story that surrounded them. Successful DNA analysis was unlikely due to the age of the items and proved to be with no DNA being found.</p>
	
	

Student	Yoram Goedhart
<i>Research carried out at</i>	Rijksmuseum
<i>Supervisor</i>	dr. Katrien Keune
<i>Title thesis</i>	Identification of possible human biological traces found on 18th century clothing
<p data-bbox="177 472 288 506"><b>Abstract</b></p> <div data-bbox="204 577 705 1160">  </div> <p data-bbox="196 1182 705 1216"><b>Breeches (ca. 1750) under forensic investigation</b></p> <div data-bbox="188 1317 821 1592">  </div> <p data-bbox="196 1608 813 1659"><b>Infrared spectrum of skin remains found on the breeches, indicating lipids on the left (2921 and 2852 cm<sup>-1</sup>) and protein on the right (1630 and 1538 cm<sup>-1</sup>)</b></p>	<p data-bbox="882 477 1414 2013">It is not uncommon for museums to have objects in possession with unknown origin or lack of clarity about what happened with the object through time. Solving this issue requires a reconstruction of events and truth-finding that shows overlap with the investigation of a crime scene. Therefore, a forensic approach may be of help within cultural heritage. However, there is little knowledge on whether the forensic approach can successfully be applied to objects that are multiple centuries old. Therefore, the current study will explore to what extent a modern forensic approach can contribute to the documentation, identification and analysis of highly fragmented and aged materials in a case of cultural heritage. To reach this goal, a forensic trace investigation was conducted on a pair of 18th century breeches, that have been retrieved from an anonymous grave on Spitsbergen. These breeches contain unidentified materials, among which possibly human traces. Trace material was examined using a microscopy-based approach. It appeared that the breeches contained mainly traces of biological origin. Using a small selection of trace material, Energy-dispersive X-ray (EDX) and Attenuated Total Reflection Fourier Transform Infrared (ATR-FTIR) spectroscopy indicated the presence of human skin remains. It was concluded that a modern forensic approach can successfully be applied to a historical object within cultural heritage and can help decision-making regarding possible future conservation of the object. The systematic documentation of the forensic methodology was found to be appropriate with little to no modification. Regarding analysis and identification, the forensic approach appears suitable to classify and identify trace materials, but has room for improvement. The current work can be a starting point that allows for more questions regarding museum objects to be answered.</p>