

**SPRING 2020
CHEMISTRY
SEMINAR SERIES**



**DR. CATHERINE
GRGICAK**

Department of Chemistry
Rutgers University
Camden, NJ

**HOST:
DR. BRENNER-MOYER**

**COFFEE SOCIAL
11:00 AM
OLSON HALL, 338**

**ALL THOSE
INTERESTED ARE
WELCOME TO ATTEND**

RUTGERS
UNIVERSITY | NEWARK

Department of Chemistry
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<https://sasn.rutgers.edu/chemistry>

**“FORENSIC DNA DECONVOLUTION PROBLEMS AND
SOLUTIONS THEREOF”**

**March 6th, 2020 ~ 11:30AM
Life Science Center II, Room 130**

Abstract: Forensic DNA signal is notoriously challenging to interpret and requires the implementation of computational tools that support interpretation. While data from high-copy, low-contributor samples result in electropherogram signal that is readily interpreted by probabilistic methods, electropherogram signal from forensic stains can consist of low-copy, high-contributor-number samples that are often obfuscated by peak-sharing, false non-detections, artifacts and noise, all of which greatly complicate interpretation. Since forensic DNA profiles are too complicated to quantitatively assess by standard statistical methods, continuous probabilistic frameworks have been developed to draw inferences on the Number of Contributors (NOC) and the Likelihood Ratio (LR) of the electropherogram given the prosecution and defense's hypotheses.

In this work we present the validation of a new version of the NOCIt inference platform that determines an A Posteriori Probability (APP) distribution of the number of contributors given an electropherogram. NOCIt is a continuous inference system that incorporates models of peak height (including models of DNA degradation), shadow-band artifacts, noise and peak non-detection while taking into account allele frequencies in a reference population. We established the algorithm's performance by conducting tests on samples that were representative of types often encountered in practice. In total, NOCIt's performance was tested using 815 degraded, UV-damaged, inhibited, differentially degraded, or uncompromised DNA mixture samples containing up to 5 contributors. We found that the model makes accurate, repeatable and reliable inferences about the NOCs and significantly outperformed methods that rely on signal filtering.

By leveraging recent theoretical results of Slooten and Caliebe (FSI:G, 2018) that, under suitable assumptions, establishes the NOC can be treated as a nuisance variable, we further demonstrate that when the APP is used in conjunction with a downstream likelihood ratio (LR) inference systems that employs the same probabilistic model, a full evaluation across multiple contributor numbers is rendered. This work, therefore, illustrates the power of modern probabilistic systems to report holistic and interpretable weights-of-evidence to the trier-of-fact without assigning potentially erroneous numbers of contributors or filtering signal.

Biographical Sketch: Catherine Grgicak (Gerg-i-chuck) is an Associate Professor and Henry Rutgers Chair in the Department of Chemistry at Rutgers University in Camden NJ. Previous to joining Rutgers, she was an Assistant Professor at Boston University's Program in Biomedical Forensic Sciences where she and her long-run collaborators developed methods by which to interpret the most complex mixed and partial signal using Bayesian statistics and probability theory. She received her B.S. in Physical Sciences and B.Ed. from the University of Windsor, her M.S.F.S. from the University of Alabama at Birmingham, and her Ph.D. in Chemistry from the University of Ottawa. Her Laboratory for Forensic Technology and Integration is a research laboratory focused on the development of systems and procedures to improve forensically relevant bio-analytical processes. She is Executive Secretary of NIST's OSAC Committee on Biology and is a member of the Journal of Forensic Science's editorial board, the American Society of Forensic Sciences, the International Society of Forensic Genetics and the Center for Computational and Integrative Biology at Rutgers University.