Risk-based Conflict Predictions for Large Trucks Merging in Work Zones

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Keywords: Large Trucks, Merging Decision, Risk Assessment, Surrogate Safety Assessment, Work Zones

Abstract- Trucks play a significant role in accidents in work zones. Large trucks and other commercial motor vehicles (CMVs) were involved in more than 33% of fatal collisions in work zones in 2021. Large trucks are involved in about 30% of work zone collisions, according to the Federal Highway Administration (FHWA). One of the reasons for truck-related conflicts in the work zone is its size. When a truck merges in a lane already in use, it may cause a risk of conflicts with other vehicles and raise the possibility of crashes. To assist large trucks trying to merge into a traffic stream in the advanced warning area and transition area in work zones, this study measures the conflict risk associated with work zone merging and creates a decision strategy based on that assessment. Microscopic driving data is collected from a microscopic traffic simulation software, SUMO, for large trucks merging in a work zone. The data is preprocessed and labeled based on a surrogate safety measure, time to collision (TTC). A statistical model is trained with this data that predicts the probability of prior risk of trucks merging into a mixed traffic stream in a work zone. A truck intending to merge and its immediate downstream vehicle in the target lane must leave a minimum safe space, which is satisfied by this risk-based merging approach. This developed method has real-world applications. A traffic video camera can be placed on the roadside of work zones' advanced warning areas and transition areas, where the camera captures the video. The camera is connected to a roadside computing unit that can detect vehicles, their speeds, accelerations, heading directions, positions, and relative distances. Based on the pre-trained statistical model, the roadside computing unit predicts the conflicts and sends alerts to the trucks under risky conditions. The trucks are equipped with 5.9 GHz communications radios by which they receive the alerts. This work also measures the end-to-end latency and scalability of the developed method under different weather and lighting conditions to study its feasibility.

Automated Analysis of Cardiovascular System Using Deep Learning

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Presentation Keywords - vasculature segmentation; deep learning; image segmentation; peripheral arterial disease; vascular calcification

Abstract: Atherosclerosis, a chronic inflammatory disease affecting the arteries in the cardiovascular system, presents a global health risk. Accurate analysis of diagnostic images, like computed tomographic angiograms (CTAs), is essential for staging and monitoring the progression of atherosclerosis-related conditions, including peripheral arterial disease (PAD). However, manual analysis of CTA images is time-consuming and tedious. To address this limitation, we employed a deep learning model to segment the vascular system in CTA images of PAD patients undergoing femoral endarterectomy surgery and to measure vascular calcification from the left renal artery to the patella. Utilizing proprietary CTA images of 27 patients undergoing femoral endarterectomy surgery provided by Prisma Health Midlands, we developed a Deep Neural Network (DNN) model to first segment the arterial system, starting from the descending aorta to the patella, and second, to provide a metric of arterial calcification. Our designed DNN achieved 83.4% average Dice accuracy in segmenting arteries from aorta to patella, advancing the state-of-the-art by 0.8%. Furthermore, our work is the first to present a robust statistical analysis of automated calcification measurement in the lower extremities using deep learning, attaining a Mean Absolute Percentage Error (MAPE) of 9.5% and a correlation coefficient of 0.978 between automated and manual calcification scores. These findings underscore the potential of deep learning techniques as a rapid and accurate tool for medical professionals to assess calcification in the abdominal aorta and its branches above the patella. Please visit this paper GitHub page at https://github.com/pip-alireza/DeepCalcScoring.

ADAPT in SC: Utilizing Change Point Detection for Structural Dynamic Response Classification

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Keywords: Change point detection, structural systems, time series, structural health monitoring

Change point detection mechanisms offer the ability to classify the dynamic response of structures subjected to shock and vibration events. Grounded in the premise that structural systems undergoing continuous vibrations exhibit distinct behavioral shifts when encountering shock events, this paper introduces a framework for leveraging change point detection algorithms to analyze time series data from vibrational sensors. This approach is predicated on the hypothesis that significant changes in the data's statistical properties—such as mean, variance, and frequency—can effectively signal the onset and cessation of shock states, thus providing a clear demarcation of structural response phases. The study outlines the process of implementing various change point detection algorithms, including both parametric and non-parametric methods, to identify critical transitions within vibration data. The effectiveness of these algorithms is evaluated through a series of experiments involving both simulated and real-world structures subjected to controlled impact tests. Future directions are suggested for integrating change point detection with other analytical techniques to enhance the predictive capabilities of structural health monitoring frameworks.

Predicting Customer Status through Bayesian Networks with Imbalanced Data Handling

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Keywords:

Probabilistic Graphical Model, Bayesian Networks, Imbalanced Data, Validation, and Evaluation Metrics

Abstract:

Our project focuses on predicting customer status for a South Carolina company using Probabilistic Graphical Model (PGM) while addressing challenges associated with imbalanced data through different sampling methods. The project's objective is to enhance the accuracy and reliability of predictions, especially in scenarios where imbalances in the dataset could impact the model's performance. We will introduce Bayesian networks, a type of PGM and the implementation of k-fold validation. Explorations into evaluation metrics provide a nuanced understanding of the model's performance. The final stages of the project involve creating graphical representations of key metrics, exploring UnderSampling and OverSampling techniques. The research contributes valuable insights into predicting customer status, particularly in the context of imbalanced data, with the outcomes and methodologies poised for discussion and application in practical settings.

Biographical Sketch

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Bhakti Patel, a senior majoring in Computer Science and Mathematics, harbors a profound interest in artificial intelligence and full-stack web development. Through internships at a local South Carolina Hospital and research collaboration with local South Carolina company, Bhakti has honed a versatile skill set encompassing ASP.NET, C#, Python, and Bayesian networks. Notable achievements include contributions to patient workflow optimization and customer status prediction. Concurrently, Bhakti actively contributes to her math capstone project and currently implements logistic regression for data analysis. Actively engaged in academic organizations like Upsilon Pi Epsilon, Kappa Mu Epsilon, and ACM, Bhakti boasts a 3.90 GPA and demonstrates leadership qualities. Noteworthy projects such as the Math Hub application underscore Bhakti's proficiency in full-stack development and Agile methodologies. Bhakti's presentations at conferences like NCUWM Conference and Math Fest attest to her adeptness in effective communication and offering valuable insights.

Hyperspectral Image Classification of Bacteria Using a Convolutional Neural Network

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Keywords Hyperspectral Imaging, Convolutional Neural Network, Bacterial Classification, Deep Learning

Introduction: The goal is to grow and identify marine microbes using a combination of hyperspectral imaging and deep learning. Hyperspectral imaging (HSI) allows for us to image the target sample and collect both spatial information and spectral information to generate a 3D map of the distribution of various bacterial types. The Whiskbroom HSI method has been used to acquire data point by point in micrometer intervals along with each point being imaged at multiple wavelengths.

The image that is generated from the reflected beam with a wide spectrum can be processed using the PyTorch deep learning library in Python. Deep learning is important for hyperspectral image classification of bacteria because of amount of wavelengths in the visible spectrum and near infrared spectrum being used as well as the powerful feature selection and feature extraction tools of deep learning. For this project, Python has been used because there are several libraries for image analysis and image processing with deep learning such as PyTorchand Sklearn. Once the files are input into the supervised deep learning model, they will be broken down into their respective images and fed through the network. Training occurs over several iterations to generate a probability that indicates the bacteria type.

Materials and Methods: The setup used involved an NKT Superk-Fanium-OCT 6 laser with a spectrum ranged from 390 to 2400 nm, a Varia filter that selected the spectrum of the laser from 550 to 850 nm, beam splitters, collimators, lenses, a fiber output coupling, a Galvo scanner, and a linear CMOS camera to record the spectral data. The sample surface was scanned rapidly while the reflected spectrum was recorded by the camera. The images were processed using a supervised deep learning model.

There was a total of 443 input files, which were 2048×4096 pixels with each row being an individual image. This means that each file was 2048×4096 pixel images for a total of 907,264 images. The deep learning model consisted of 2 1-D convolutional layers, 2 pooling layers, and one fully connected layer. The LeakyReLU function was used for each layer along with each layer using a dropout function. The images were then normalized to set pixel intensity values between 0 and 1. The files went through a stage of preparation and preprocessing prior to being input into the model. This step involved splitting the input images with an 80/20 training/validation split where 80% (117,964) of the images were randomly selected to be used for training and the remaining 20% (29,492) being used to validate the model.

A hyperparameter sweep using the Hyperopt library was run to determine the best options for maximizing the F1 score which is used to monitor how well the model does at minimizing both false positives and false negatives. After 100 iterations and 27 hours of testing different combinations of parameters using the Tree-Structured Parzen Estimator with Hyperopt, a batch size of 256, dropout rate of roughly 0.2511, learning rate of roughly 0.0016, weight decay of roughly 6.9213e⁻⁰⁶, kernel sizes of 5, pooling sizes of 2, and 64 kernels for both convolutional

layers were determined to yield the maximum F1 scores. The model was trained over 10 iterations and was done by having the image input into the model while in training mode where both dropout and normalization occurs. The gradients were zeroed out and a forward pass was performed. Once predictions were made, the loss was computed using BCEWithLogitsLoss to measure how far off the predictions were from the correct labels. Backpropagation was performed with the Adam optimizer to update the learnable parameters. The model then switched to evaluation mode and another forward pass was performed without. The outputs were passed through a sigmoid function to obtain probabilities with a threshold of 0.5 being used to convert probabilities to labels. Predicted and true labels are stored to compute F1 scores. The bacterium types being classified were referred to as ATL 1, ATL 3, ATL 28, and B 27.

Results: With the imaging setup, 4 different types of bacteria were able to be classified. F1 scores and loss were calculated to determine how well the model performed. After 10 runs, an average F1 score of 0.9578 was obtained for ATL 1, 0.9575 for ATL 3, 0.9348 for ATL 28, and 0.9245 for B 27. An average training loss of 0.1310 and an average validation loss of 0.0872 was recorded from 10 runs.

Discussion and Conclusions: The Whiskbroom HSI method was successfully used along with a supervised deep learning algorithm to collect the data, prepare, and preprocess the signal, and classify the image as a certain type of bacteria based on the recorded spectrum. While this method was used only to identify and classify 4 different types of bacteria, our preliminary data demonstrates that the approach can perform both feature selection and feature extraction on hyperspectral images ranging from 550 to 850 nm.

ADAPT in SC- Comparison of ML Algorithms to Classify Microscopic Biological Particles

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Presentation Keywords: Machine Learning, Classification, Microscopic Biological Particles

Introduction: Impedance Flow Cytometry (IFC) has become a popular method for characterizing a variety of microscopic biological entities, including different cell types, waterborne parasites, bacteria, and bacterial spores. Its appeal lies in its label-free approach and minimal sample preparation requirements. A popular IFC design features a pair of facing or coplanar electrodes embedded in a microfluidic channel. These electrodes are energized with a voltage at one or more discrete frequencies, creating an electric field within the channel. As a cell passes through the channel, fluctuations in electric current are detected, thus providing the impedance of the individual cell. The impedance signal offers significant insights into the measurement of biological particles, and thus, impedance-based classification can be used in many areas, such as disease diagnosis and food safety control. However, due to the heterogeneous populations and complex dataset, it is challenging to classify the particles accurately and efficiently through manual analysis or simple statistical methods. As a result, different machine learning algorithms have been applied to improve the accuracy and efficiency of impedance-based datasets. For example, Zhang et al. developed a deep learning assisted microfluidic impedance flow cytometry for foodborne bacteria analysis and classification, Xu et al. reported an impedance detection of *E. coli* with supporting vector machine (SVR) algorithm, and Wang et al. applied decision-tree algorithm for qualitative and quantitative analysis of three bacteria based on their impedance signal. Although many researchers have attempted to apply various machine learning algorithms to impedance flow cytometry datasets, there is a noticeable lack of comprehensive comparative studies evaluating the efficacy of these different algorithms. This gap in research is significant, as it leaves unanswered questions about which machine learning strategies might be most effective for specific applications in impedance flow cytometry. Here a systematic comparison of these algorithms on the impedance flow cytometry datasets has been reported. This study could guide researchers in selecting the most appropriate machine learning tools for their specific impedance-based classification tasks, ultimately enhancing the accuracy, efficiency, and applicability of impedance flow cytometry in various fields.

Methodology: We developed and compared six popular Machine Learning algorithms in order to determine which one achieved better results for classifying the microscopic biological particles. In particular, we contrasted: Support Vector Machine (SVM), Decision Trees, Random Forest, Neural Networks, k-Nearest Neighbors (k-NN), and Logistic Regression. Each algorithm was applied to a standardized set of impedance flow cytometry data for parasitic protozoa. The data were preprocessed to ensure compatibility with each algorithm, including normalization and feature selection. Performance metrics, such as accuracy, precision, recall, and F1 score, were used to evaluate the efficacy of each algorithm. **Results:** The analysis revealed less variability in algorithm performance than expected, given the relatively small and simple nature of the dataset. The Decision Tree and Random Forest algorithms excelled, demonstrating high accuracy, recall, and F1 scores, suggesting they are particularly well-suited to this dataset. The Neural Network and Logistic Regression models also performed well, suggesting that even with a simpler dataset, these algorithms can be effective.

The k-Nearest Neighbors (k-NN) showed slightly lower metrics, yet still achieved high accuracy, indicating its usefulness for quick, interpretable results in smaller datasets. The Support Vector Machine (SVM) with a linear kernel performed modestly and could benefit from hyperparameter tuning to optimize its performance.

Conclusions: This study highlights the importance of algorithm selection in classifying data from impedance flow cytometry, even when dealing with smaller and less complex datasets. It shows that ensemble methods like Random Forest and Decision Trees can provide high accuracy and are easy to interpret, which is advantageous for smaller datasets. Meanwhile, Neural Networks and Logistic Regression prove to be robust alternatives. The comparative underperformance of k-NN and linear SVM in this context emphasizes that even for simple datasets, the choice of algorithm can significantly impact the results. As we look to the future, our work will focus on analyzing the impedance of nano-scaled biological particles, like exosomes, utilizing the most suitable machine learning algorithm. This advancement could open new avenues in nanobiotechnology and provide deeper insights into the intricate world of these tiny yet significant biological entities. Extending this research to include more algorithms and larger, more diverse datasets could further enhance our understanding of the optimal application of machine learning in impedance flow cytometry.

Densification and microstructure evolution of alumina samples processed via Direct Ink Writing

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Presentation Keywords: Additive manufacturing, slip-casting, Alumina, porosity, sintering.

Abstract:

Additive manufacturing of ceramics has gained widespread attention enabling the fabrication of ceramics with complex geometries. Direct Ink Writing (DIW) also called Robocasting, is an extrusion-based technique that uses a slurry with non-Newtonian viscosity and has been able to print at room temperature. The slurry must possess shear-thinning behaviour to flow through small diameter nozzles and must show a dilatant behaviour upon releasing from the nozzle. The characteristics of the initial powder and the additive manufacturing (AM) technique used in the early stages lead to the formation of a unique green structure. This structure exhibits inherent anisotropy at macro- and micro-scale, distinguishing it from conventionally processed green bodies. In this study, we have investigated the differences in the densification kinetics and microstructure evolution of samples made via slip-cast and robocast processing techniques. A slurry with optimised solid content of 55 vol% Alumina was prepared in distilled water. The slurry was printed using a robocaster from Robocasting LLC. A 50 vol% Alumina slurry was prepared in distilled water and samples were prepared via slip casting to compare those with the robocast samples. Both the samples were sintered in air at 1000, 1100, 1200, 1300 and 1400 ⁰C for 2 hours. A density measurement and microstructure analysis using SEM were performed for all the samples and compared for both the techniques. The kinetics of densification as a function of temperature and time using a dilatometer are underway to develop a kinetic model for the densification of AM produced green components.

Creating a Comprehensive Dataset to Explore Retroreflectivity Degradation in Traffic Signs: Incorporating Environmental Factors

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Keywords: Retroreflectivity, Traffic signs, Road safety, Environmental factors

Abstract

Retroreflectivity significantly impacts road safety, especially in low-light conditions and adverse weather, compromising the legibility, visibility, and comprehension of signs by road users. The deterioration of retroreflectivity over time due to aging and exposure to environmental conditions leads to reduced effectiveness, potentially resulting in road crashes and significant financial losses for road agencies. While previous studies have examined various factors contributing to retroreflectivity degradation, including signage, color, orientation, and weather conditions, there remains a gap in understanding the influence of additional environmental factors such as air temperature, relative humidity, air pollution, and orientation to the sun.

Our research aims to bridge this knowledge gap by compiling a comprehensive dataset that includes additional environmental factors such as air temperature, relative humidity, air pollution, orientation to the sun, and corresponding images of traffic signs. To achieve this, we will employ a hand-held reflectometer to measure retroreflectivity, record pertinent sign attributes, and gather real-time information on weather conditions, air pollution levels, air temperature, and relative humidity. By integrating field data with desk data, we will create a comprehensive and robust dataset that can be leveraged for future analysis and research purposes. The results of this study will not only assist transportation agencies in effectively maintaining traffic signs to improve road safety but also contribute to advancing research in retroreflectivity prediction using deep learning models. The dataset generated will serve as a valuable resource for future studies investigating the complex interactions between environmental factors and retroreflectivity degradation, ultimately enhancing our understanding of how to prolong the lifespan and effectiveness of traffic signs.

Animal Movement Patterns' Effect on Density Estimations Using Camera Traps

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Keywords: density estimation, animal movement patterns, camera traps, agent-based modeling

Introduction:

Large mammal populations are rapidly declining across the globe. As large mammals disperse and predate seeds, create habitat for other organisms, and influence vegetation structure and drive nutrient availability, their decline or extirpation can have devastating impacts on the ecosystem (Pringle et al. 2023; Villar and Medici, 2021; Villar et al. 2021). Therefore, monitoring large mammal populations is of critical importance. As quantifying population in absolute numbers provides unique challenges, population density is often used as a metric for evaluating population status and change over time (e.g. Li et al. 2023). For large mammals, camera traps are often used to determine animal presence, the results of which are incorporated into and two common models: the REM (Random Encounter Model) and REST (Random Encounter with Staying Time) model to estimate population density (Palencia et al. 2021). However, it remains unclear whether the various ways in which animals move or pass through the camera frame influences density estimates. Here, we created a model to evaluate how various animal movement patterns influence population density estimates using REM and REST models. Specifically, our model analyzed the impact of animal movement type, movement speed, animal staying time in the frame, and camera detection angles on population density estimates.

Methods:

We modeled a world with camera traps in NetLogo (an agent-based modeling program) in which individuals moved according to one of the three movement patterns: Brownian movement, Levy flight, and Ornstein-Uhlenbeck (OU). For each type of movement, the model outputs both a REM and REST estimate based off of parameters measured, giving us a set of simulated estimates for each movement pattern. Secondly, sensitivity analyses were performed on parameters (i.e. size of world, number of cameras, simulation length, individual movement parameters) to determine, within each type of movement, which estimate was more/less sensitive to changes in said parameters. These parameters were set to various levels and were each run to generate suitably rich sets of simulated data estimates. These sets of data were compared to each other using ANOVA and Kruskal-Wallace tests in R. The p-values returned in these tests served as indicators of the impact that the changes in the parameters had on the estimates.

plots generated of the data to test for normality and a division of variances to test for equal variances between datasets.

Results:

Our results indicate that changes in, number of cameras (REM $p = 2.1 \times 10^{-7}$, 5×10^{-9} , and 0.42 and REST $p = 2.2 \times 10^{-7}$, 6.2×10^{-7} , 0.13 for Brownian movement, Levy flight, and OU motion, respectively), and simulation length (REM $p = 4.9 \times 10^{-11}$, 4.2×10^{-9} , and 0.1, and REST $p = 6.2 \times 10^{-10}$, 1.6×10^{-10} , and 0.3 for Brownian movement, Levy flight, and OU motion, respectively) do create significant differences within each movement category. In other words, the type of animal movement influences the population density estimate. However, some of these movements and estimates are less sensitive than others. We also discovered that differences in movement patterns create differences in camera detections ($p_{min} = 2 \times 10^{-16}$), staying time ($p_{min} = 2 \times 10^{-16}$), speed ($p_{min} = 2 \times 10^{-16}$), REM estimate ($p_{min} = 2 \times 10^{16}$), and REST estimate ($p_{min} = 6.3 \times 10^{-8}$).

Conclusions:

We can use this information to determine which estimate is best to use in the real world based off of which world parameters we are least certain about or that could have the highest level of error or variance from test to test. We can also determine which models of animal movement translate best to each type of density estimate. This is helpful because researchers can make a justified decision about how to estimate density using camera traps by showing which type of parameter categories that their particular research zone occupy, then using the model that results in the least amount of sensitivity and error in simulated estimates for those particular world cases. Also based off of world conditions, researchers can determine which model of movement that animals might be inclined to follow for most of their time in the research period, then use the model that comes closest to the real density for that type of movement. To further this research, we hope to create a real-world long-term study at a local nature preserve to gain insight into how animal patterns and density estimates change over time observationally. From this, it may be possible to create a type of algorithm that could tell a researcher that, based on conditions provided by the researcher themselves, a particular estimation model should be used. Another possible advancement is to analyze a third estimation method that exists and is well-credited to increase the scope of the existing analysis to be more applicable.

Silicon oxycarbide/reduced graphene oxide composite anodes for lithium-ion batteries with enhanced electrochemical performance

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Keywords: SiOC, reduced graphene oxide, composite, battery

Abstract:

Silicon oxycarbides (SiOCs) have attracted attention due to their outstanding theoretical capacities and structural stability owing to their application in lithium-ion batteries (LIBs). The low electronic conductivity of SiOCs, however, has adversely affected their overall performance, therefore limiting their practical use in Li-Ion batteries. To address this, we engineered high-performance anodes by creating a hierarchical interconnected configuration of silicon oxycarbide integrated within a chemically modified reduced graphene oxide matrix, utilizing the surface modification capabilities of reduced graphene oxide for SiOC. In particular, the SiOC/rGO anodes exhibit a high initial reversibility. The capacity of this battery is approximately 1000 mA h/g at 0.37 A/g (0.1 C for graphite), exceeding that of conventional SiOC batteries. In addition, the composite anodes exhibit a considerable capacity of 700 mAh/g at 0.744 A/g (2 C for graphite) even after 800 cycles, highlighting excellent long-term cycling stability and high capacity at high rate. In addition to improved electronic conductivity, shortened ion diffusion length, and reduced chargetransfer resistance, composite structures provide enhanced electrochemical performance. SiOC/rGO composite anodes present a promising development for the commercialization of lithium-ion batteries due to their high rate of cycling and long cycle life. A range of spectroscopic, microscopic, and electrochemical techniques have been utilized in this study to characterize the materials and to understand how the batteries perform.

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