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P1 - MACHINE LEARNING AND HEALTHCARE
MACHINE LEARNING TO PREDICT SEVERE ACUTE PANCREATITIS

UOA Scientific Summer Research Special
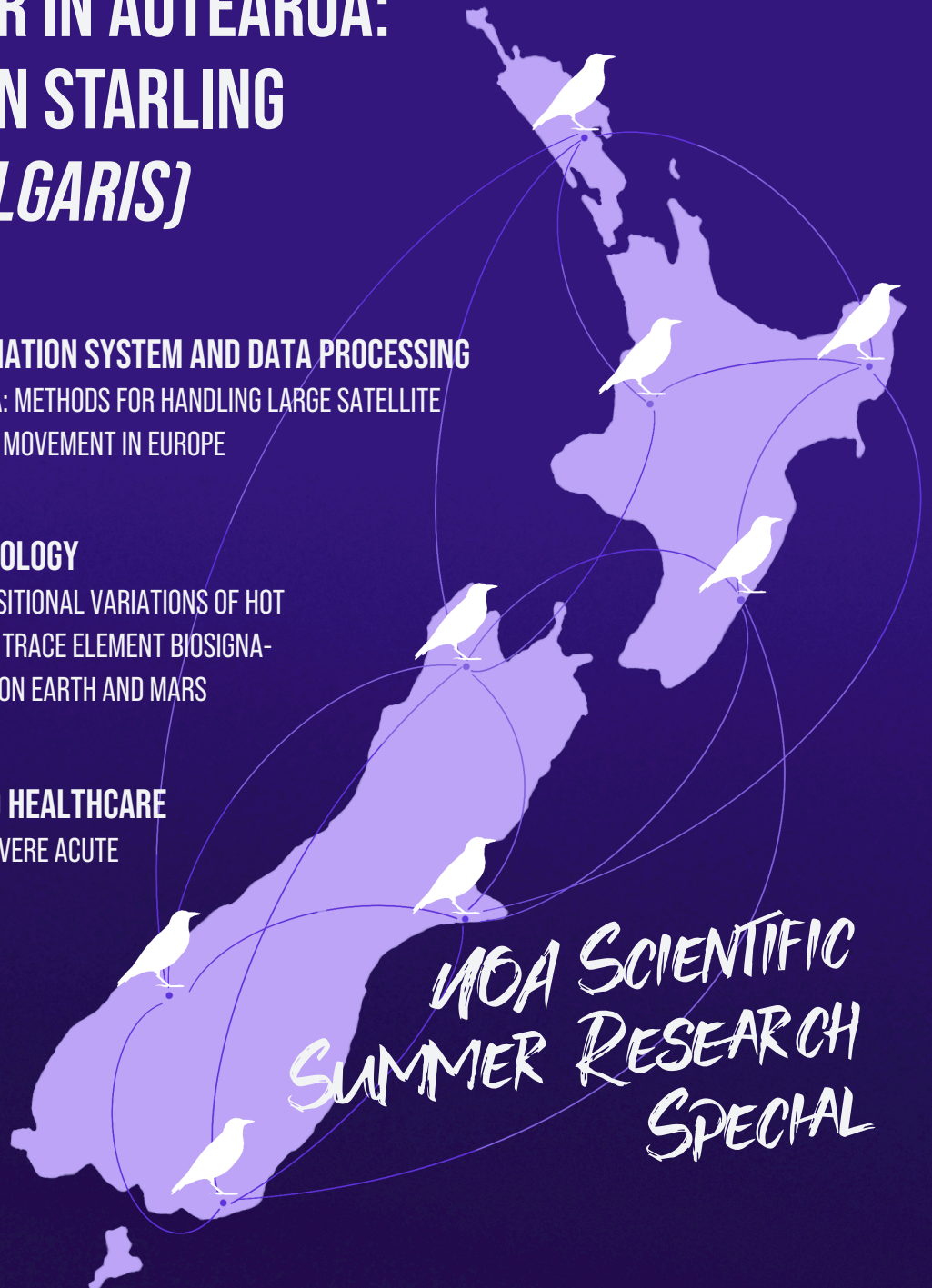
Editors' Note

Kia ora koutou katoa and welcome to the first edition of Volume 4, our summer research special!

This edition highlights some of the important research being done by students and supervisors at the university, with widereaching implications.

AI's impact is contentious. Yet in many fields, such as medicine, it holds enormous potential. In particular, Natalie Lau explores various AI models and their potential to predict the severity of acute pancreatitis. Of course, AI also brings its own challenges, including potential bias at several stages of development. Kejun Dai compares a selection of bias evaluation frameworks, considering cross compatibility and ease of use, among other metrics.

Switching it up a little, Dominique Stallard researches hot spring deposits and their possible insights into early life on Earth and Mars, while Grace Zhao and Ethan McCormick examine the interaction between crisis framing and conservation in Aotearoa New Zealand. Also focusing on the challenges to our native wildlife, Bryan Thompson characterises the genetic population structure of the invasive European Starling. Further afield, Adele Gao investigates the relationship between an eagle's flight path and changes in the wetlands of Europe's Polesia region.

Thank you so much to our writers for starting off Volume 4 with a bang! We hope you enjoy the range of articles included in this issue and keep an eye out for our future editions.

Ngā mihi nui,
Kevan Lew, Writing Coordinator for UoA Scientific, 2024

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Original Research
Machine Learning to Predict Severe Acute Pancreatitis

Natalie Lau

Machine Learning and Healthcare

Data-driven machine learning methods promote evidence-based decision-making in multiple industries, including healthcare, where machine learning techniques have improved the accuracy of predicting and preventing health complications. This research focuses on utilising machine learning techniques to predict severe acute pancreatitis. Currently, clinical scoring systems are used by health professionals in hospitals to quantify the severity of acute pancreatitis. However, these scoring systems have limitations. This research uses routinely collected patient data to train, predict, and validate several machine learning models. It is shown that the accuracy of predicted results from machine learning algorithms is better than those of the clinical scoring systems.

Acute pancreatitis (AP), an inflammatory disorder of the pancreas associated with substantial morbidity and mortality, is one of the most common gastrointestinal causes of hospital admission in the USA [1]. In New Zealand, AP continues to have a high incidence rate, with Māori patients reporting the highest incidence of AP (per 100,000 people per year) worldwide [2]. While AP-related mortality has decreased over the past decade, likely due to technological advancements and improvements in timely and accurate diagnoses, morbidity and its consequences remain substantial.

To manage, evaluate, and predict the severity and mortality of AP, current clinician practices include evaluating clinical data. This involves assessing organ function, conducting laboratory tests and imaging, and utilising clinical scoring systems. Examples of clinical scoring systems to assess the severity of AP include Acute Physiology and Chronic Health Evaluation II and the Glasgow-Imrie Criteria. While existing literature provides insight into the quantification of the severity of AP based on these clinical scoring systems, studies have shown that these systems only offer some-encompassing prediction methods, leaving much room for improvement [3]. Evidence from several studies indicates significant differences in the accuracy of these scoring systems in forecasting the severity, local complications, organ failure, and associated mortality of AP [4]. The lack of uniform standards and the degree of inconsistency among the scoring systems provides an opportunity to develop new, more robust scoring systems.

Data-driven machine learning methods promote evidence-based decision-making in multiple industries, including healthcare, where machine learning techniques have improved the accuracy of predicting and preventing health complications. In particular, studies have been conducted regarding using machine learning in predicting the severity of AP. For example, Andersson et al. [5] present a machine learning-based study using data from 200 patients with 23 potential risk variables. Additionally, EASY-APP [6] is a machine learning-based, user-friendly web application developed using an international cohort of nearly 5000 patients. It is the first model made available and used by clinicians.

The severity level of AP is classified using the Revised Atlanta Classification (RAC). RAC is considered the global consensus classification of AP, which classifies the severity of AP as mild, moderate, or severe [7]. Mild AP describes no organ failure or local or systemic complications and is usually resolved within the first week. Moderate AP describes the presence of transient organ failure, local complications, or exacerbation of co-morbid disease. Severe AP describes persistent organ failure.

Method

Figure 1 provides an overview of the machine learning pipeline used in this research. The components are described in the following subsections.
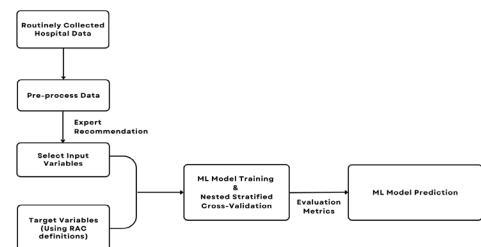
Figure 1: An overview of the machine learning pipeline used in this research.

Data

This study uses a retrospective dataset comprising patient data from 2009 to 2013 in a mainland Chinese hospital. Adult patients admitted to the hospital and diagnosed with AP, as per the 2012 updated Atlanta criteria, were included in the study. The dataset contains 2,581 deidentified patient data with more than 50 variables, including diagnoses, decisions, vital signs, routine laboratory test results, and calculations using scoring systems. The dataset also includes the patient level of AP for patients, categorised using RAC, and comprises 65.2% male and 34.8% female patients, with an average age of 47.2 years and an age range of 18 to 80 years. Figure 2 provides an overview of the distribution of data based on the age and gender of patients.

Among 50+ variables, 34 features were selected through expert recommendation. These included risk factors such as patient's gender, age, and abdominal pain onset time; triage information such as high dependency unit and intensive care unit; and vital signs including temperature, respiration, and heart rate. Information on organ failure, the site of the organ failure (lung, kidney, heart, etc.), and selected variables from the laboratory test results were also included.
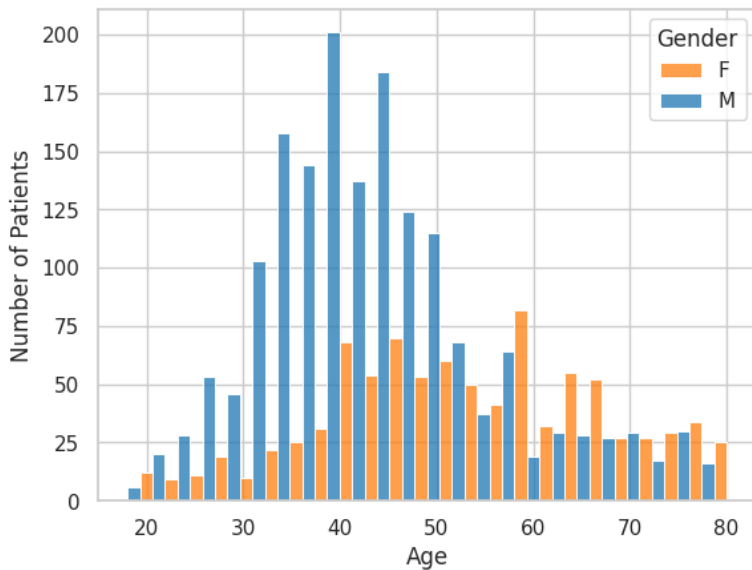
Figure 2: Distribution plot of the total number of patients based on their age group and gender.

Target Variables

To predict the severity of AP, this research uses the definitions of RAC which categorise the disease into mild, moderate, or severe. Binary classification tasks with two classes were formed by combining the RAC subgroups, where moderate and severe are one class, and mild is the second class. The formation of binary classes provides the opportunity to compare with the clinical scoring systems directly.

Machine Learning Algorithms and Evaluations

This research uses three machine learning algorithms: support vector machine (SVM), random forest (RF), and XGBoost (XGB). SVM is an algorithm that assigns labels to objects from learning by example. SVM uses kernel functions to transform the input data into a higher-dimensional feature space [8]. RF is made of multiple decision trees, combining their outputs to gain a single result. RF uses bagging, also known as bootstrapping, which refers to sampling with replacement [9]. XGBoost is a scalable boosting system that builds on decision trees, ensemble learning, and gradient boosting [10].

Three evaluation metrics are discussed in this research: sensitivity (SEN), specificity (SPE), and accuracy (ACC). SEN describes a model's probability of gaining a positive result, where a high SEN indicates a reduced likelihood of missing a positive diagnosis or a lower false negative rate [11]. SPE describes a model's probability of gaining a negative result, where a high SPE indicates a reduced likelihood of misdiagnosing a negative classification, leading to a lower false positive rate [11]. ACC measures the model's ability to correctly diagnose patients, where a high ACC may indicate a useful classifier. It is a proportion of correctly classified samples in the total samples [12].

Experimental Setup

This research was implemented using Python. The sci-kit library implements the SVM and RF classifiers, and hyperparameter tuning. The XGBoost classifier, meanwhile, runs based on the XGBoost library. All experiments employ nested stratified cross-validation, reporting the

average performance of each run. We defined a fixed random seed to ensure experiments and results are reproducible. The code written for this research was executed on Jupyter Notebook.

Results

Table 1 presents results of machine learning algorithms based on RAC using binary classification. The SVM and RF models have high SPE compared to XGBoost, indicating a reduced likelihood of misdiagnosing a negative classification. On the other hand, the XGBoost model excels in SEN, suggesting that XGBoost is particularly apt for screening purposes, and can accurately pinpoint patients who are not severe cases. Overall, all machine learning models demonstrate a high level of accuracy, indicating good discrimination.

Table 2 presents the results of severe AP patients classified using clinical scoring systems. In comparison to machine learning models, as shown in Table 1, the accuracy and sensitivity of clinical scoring systems are poor, and the specificity scores are similar or slightly better. In terms of overall scoring, machine learning models appear to be comparable or better than clinical scoring systems indicating the potential of machine learning algorithms for predicting the severity of acute pancreatitis.

Discussion

This research provided experimental evidence showcasing the capabilities of machine learning algorithms predicting severe AP cases using routinely collected hospital data. We also provide a direct comparison with clinical scoring systems, where the performance of machine learning models are consistently better. This research has many future directions, including obtaining data from other hospitals for further validation of the ML models, discussions with experts to design a deployment plan, and incorporating clinician feedback.

Metric	SVM	RF	XGB
SEN	0.7109 ± 0.0258	0.7402 ± 0.0227	**0.8356 ± 0.0230**
SPE	**0.9601 ± 0.0161**	**0.9536 ± 0.0141**	0.8759 ± 0.0269
ACC	0.8181 ± 0.0129	0.8320 ± 0.0137	**0.8529 ± 0.0136**

Table 1: Machine learning models for predicting severe AP based on RAC using binary classification. Mean values with standard deviations are presented. The best scores for each evaluation metric are bolded.

Metric	APACHE II (≥8)	GLASGOW (≥3)	BISAP (≥3)
SEN	0.3038 ± 0.0178	0.3587 ± 0.0149	0.1883 ± 0.0223
SPE	0.9655 ± 0.0092	0.9532 ± 0.0091	0.9921 ± 0.0050
ACC	0.5885 ± 0.0101	0.6146 ± 0.0107	0.5342 ± 0.0127

Table 2: Clinical Scoring Systems for predicting severe AP. Mean values with standard deviations are presented.

Acknowledgements

Natalie Lau - BE(Hons)/BA, Engineering Science and Asian Studies
Natalie is a 4th year Bachelor of Engineering (Honours) and Bachelor of Arts student, majoring in Engineering Science and Asian Studies. She conducted her summer research scholarship with the Faculty of Computer Science.

How Do We Know That Artificial Intelligence Models Are Fair? An Overview of Bias Evaluating Frameworks for AI Models

Kejun Dai

Artificial Intelligence and Fairness

Artificial intelligence (AI) has become prevalent in many day-to-day decision-making processes. However, studies have found that AI models risk making discriminatory predictions. In response, bias evaluation frameworks have been developed to quantify the bias in particular models and provide methods to mitigate it. This survey examines the current state of bias evaluation frameworks and identifies possible improvements. Each framework is evaluated based on its reliability, generalisability, guidance, and robustness. My main finding is that all frameworks are restricted to address fairness as only equality, rather than equity. They also lack clarity and guidance for new users to differentiate their metrics.

Artificial Intelligence's Fairness Problem

Artificial intelligence (AI) is a developing technology that has exploded into widespread popularity in recent years. Its ability to enable machines to generate accurate decisions that can rival experts in the same fields attracts attention from many businesses and government organisations. As a result, AI models are increasingly implemented in decision-making processes, even influencing decisions that are critical to individuals' lives, such as loan approval [1], job recruits [2], school admission [3], and credit card risk prediction [4].

However, AI models must be trained with large amounts of data to extract sufficient knowledge to achieve expert-level accuracy. They are not immune to real world bias in the training data, and can make discriminatory decisions [5]. For example, COMPAS, a criminal risk assessment program, was more likely to falsely label black individuals with a high risk of reoffense than white individuals [6]. In another case, an algorithm designed to promote job advertisements in the STEM fields showed fewer ads to women than men, which was not the intention of its authors [7].

Fairness in machine learning is an emerging area of research within the wider field of AI that intends to address this issue. Current research involves developing algorithms to mitigate biases in AI models during the phases of data collection, model training, and development phases. It encompasses the development of methods and tools to help quantify bias in AI models using fairness metrics and auditing the degree of fairness with which they operate. However, the inconsistencies in model fairness are a multifaceted social problem, and researchers have not yet agreed upon a definitive set of fairness metrics. As a result, a diverse range of fairness metrics have been proposed and are used in fairness machine learning research.

Bias evaluation frameworks are tools that allow users to calculate fairness metrics of their AI models, modify these models by implementing bias mitigation techniques, and sometimes automate users' benchmark experiments.

Method

My summer research project surveyed state-of-the-art bias evaluation frameworks to identify any potential improvements that could be made in the future. My methodology involved learning each framework and demonstrating its capabilities with benchmark experiments. Then, I evaluated the different frameworks, focusing on aspects such as reliability, generalisability, guidance, and robustness. In this context, reliability refers to how unlikely the frameworks are to encounter problems during operations. Generalisability is the framework's compatibility with models and datasets from different AI ecosystems. Guidance reflects a new user's ease or difficulty in understanding and utilising the frameworks. Robustness entails the frameworks' capability to evaluate bias in different AI models.

Results

In my research survey, I encountered AI Fairness 360 [8], Fairness Indicators [9], Aequitas [10], Fairpy [11], Evaluate [12], and HELM [13]. These bias evaluation frameworks can be classified into two types: standard and subordinate (Table 1).

Standard frameworks are usually developed by researchers to allow the AI industry to adopt their findings easily. As a result, these frameworks often offer a diverse range of fairness metrics and are usually equipped with state of the art bias mitigation methods. Aequitas is the most advanced candidate among the standard frameworks thanks to its robust assessment capability. It can provide extensive catalogues of fairness metrics, including 11 absolute metrics and their group disparity. It can also help users interpret these metrics by translating them into digestible reports using threshold-based tests. In addition, it is less demanding regarding technology and workflow compatibility, meaning that it is much easier to adopt than its counterparts. One shortfall of Aequitas is that it is built to evaluate predictions from a single

	Category	Model Type	Reliability	Generalisability	Guidance	Robustness
AI Fairness 360 [8]	Standard	ML	-Transforming a large dataset into a specific data structure may cause problems -Some of its bias mitigation feature has bugs that remain	-Strictly require transforming training datasets into a specific data structure	-Multiple detailed tutorials -Demo for each bias mitigation method	-Large range of metrics - data structure is more restricted and less transformable than the popular *DataFrame* data structure
Fairness Indicators [9]	Subordinate (Tensorflow)	ML	-Restricted to much older technology -Easily cause dependency conflict with other AI ecosystem	-Can take Tensorflow models as input -In the case of non-Tensorflow models, Input requires only predictions and ground truth	-Several tutorials -However, they all do not work due to dependency conflict -Require some Tensorflow ecosystem knowledge	-For non-Tensorflow models, there are a large range of similar metrics -Visualisation is limited, making its interpretation tedious -More options for Tensorflow models
Aequitas [10]	Standard	ML	-No problems with its bias evaluation feature -Its bias mitigation feature has some problems	-Input only requires predictions and ground truth	-Extensive tutorials	-Large range of absolute and disparity metrics -Output is easy to transform and extract -Provide digestible visualisation
Fairpy [11]	Standard	LM	-Do not provide packages. You have to download the repository to install -Restricted to older technology -Most of its features do not work	-Seem to accept users' custom models -Seem not to allow users to specify dataset when calculating metrics	-No install information. Only show its major dependency. -Provide only four lines of example codes	-Large range of metrics and mitigation methods -Output is displayed on the console
Evaluate [12]	Subordinate (HuggingFace)	LM	-Some HuggingFace models are incompatible with one of the model's metrics	-Input only requires models' generation -Different metrics require different format	-A detailed tutorial	-Only three absolute metric -Different metrics have different outputs. -Easy extract outcomes from output
HELM [13]	Standard	LM	-Rely on older technologies. Because of that, it is incompatible with new HuggingFace models -Flood console with logs, making encountered problems unidentifiable	-Only accept HuggingFace models -Built-in models required users' own API access -No custom datasets	-Detailed documents for using the framework -List of interfaces that its classes provide	-Automate large-scale benchmark experiments for state-of-the-art large language models -However, its fairness metrics are relatively weak compared to other bias evaluation frameworks.

Table 1: Summary of my assessments of bias evaluation frameworks covered in the survey. ML refers to machine learning models, and LM to language models.

model, making it less convenient to evaluate multiple epochs of single or multiple models.

The other type of bias evaluation framework is the subordinate framework. These frameworks tend to be developed by a prominent actor in the AI industry, generally as their response to the fairness problem. As a result, they are small libraries belonging to a larger AI ecosystem. Subordinate frameworks usually offer only a few fairness metrics and lack features with which standard frameworks would be equipped. However, they benefit from better integration with their ecosystem than standard frameworks.
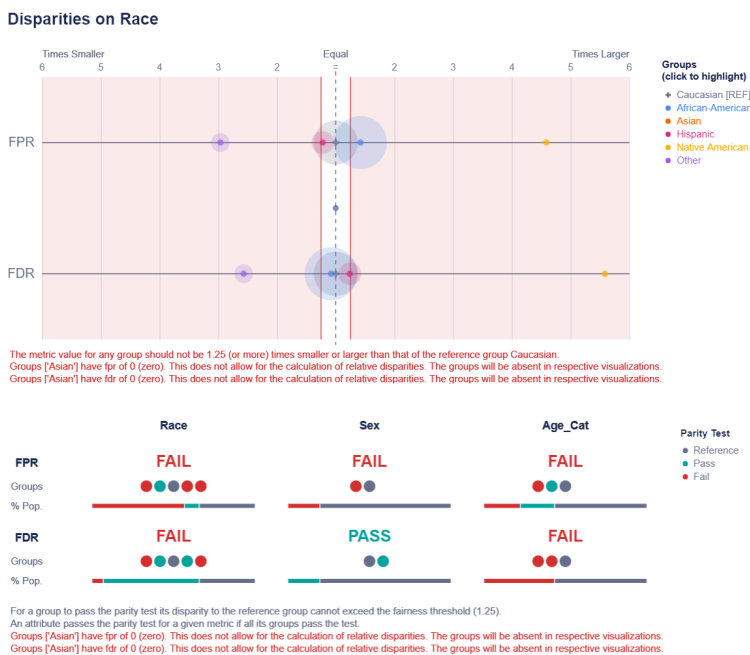
Fairness Indicators is an example of a subordinate framework. It is built at the top of the model analysis library of the Tensorflow ecosystem. Its instalment also comes with the What-If tool, which visualises the effect on

Figure 1: Aequitas' visualisation of the result of a model's evaluation [10].

Tensorflow models' performance after editing them [9]. Compared to Aequitas, it offers fewer absolute metrics and lacks their group disparity counterpart. Moreover, it only compares one fairness metric across different groups at a time, making analysing the tradeoff between models' performance and fairness metrics much more tedious. However, it provides a much more in-depth evaluation of Tensorflow models by cooperating with other libraries in the Tensorflow ecosystem [9].

Discussion

Several common problems have arisen across all bias evaluation frameworks. One is that the fairness metrics they provide are limited to definitions based on the model's prediction and ground truth. In other words, they perceive fairness as equality, rather than equity. Consequently, they may not actually contribute anything useful to the fairness problem in scenarios where equitable predictions are preferred over equal predictions.

Another common problem is that these frameworks do not provide enough guiding materials to new users regarding which fairness metrics they should employ. These frameworks all assume that users have a complete understanding of each metric's usage and limitations and can choose the best metric suited for their situations. Unfortunately, this assumption does not apply to users who are new to model fairness evaluations. The available metrics are extensive yet similar, and leave new users needing clarification and guidance when selecting between them.
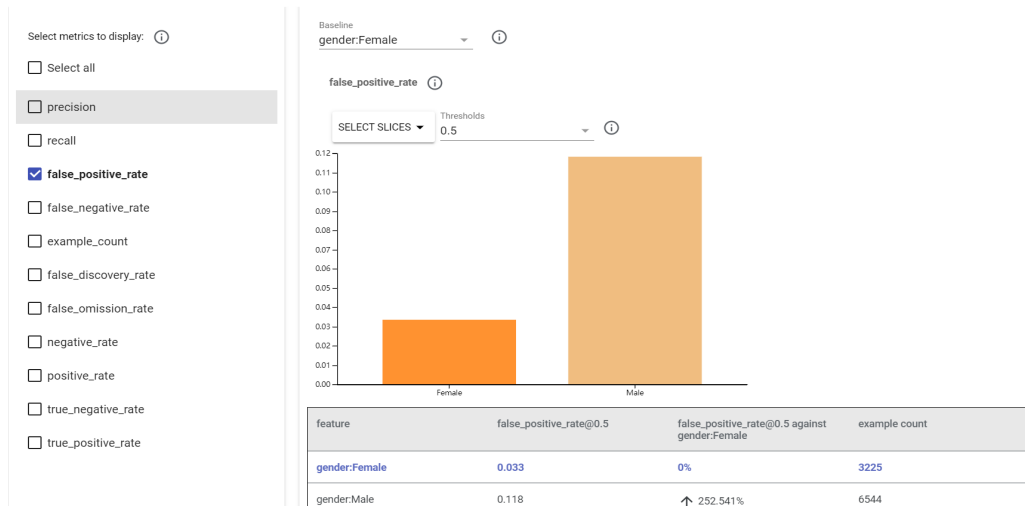
Figure 2: Fairness Indicators' visualisation of the result of a model's evaluation [9].

The future development of bias evaluation frameworks should focus on creating and utilising new fairness metrics with other definitions. According to a similar study, we can explore fairness metrics with definitions based on predicted probability, ground truth, and the similarity between predictions and causal reasoning [14]. In addition, bias evaluation frameworks should introduce new guiding materials for choosing bias metrics. These materials do not need to be extensive; even an example scenario or a short sentence suggesting the metrics' application would suffice. Another area that future development should focus on is the bias evaluation frameworks for language models. Currently, frameworks for language models are less competent than their counterparts for machine learning models. However, researchers are developing a diverse range of bias evaluation and mitigation methods [11]. It is possible to create a bias evaluation framework with the equivalent evaluating capabilities of Aequitas for language models.

In conclusion, the survey provides a brief overview of the current state of standard and subordinate bias evaluation frameworks. It also finds that most of them disproportionately treat fairness as only equality rather than equity through their rosters of fairness metrics.

Acknowledgements

Kejun Dai - BAdvSci(Hons), Computer Science

Kejun is a fourth year student interested in machine learning and its fairness dilemma. He is currently participating in his Honours project, working on utilising meta-learning to help address the dilemma.

Original Research

Exploring 'Crisis' Epistemology in New Zealand's Biodiversity Conservation Efforts

Grace Zhao & Ethan McCormick

Biodiversity and Crisis Framing

Declarations of a 'climate crisis' and 'climate emergency' have been followed by claims of a 'biodiversity crisis' which have yet to be fully explored within New Zealand. Drawing from ten interviews, we explore how crisis epistemology is constructed, and its motivations and consequences. Interviewees claim 'crisis framing' highlights the realities of biodiversity loss and invokes public action, yet has unintended consequences like eco-anxiety amongst youth and desensitisation to issues. Furthermore, many emphasise that crisis framing favours colonial power structures, overriding the rights of Indigenous peoples. Thus, we unpack the delicate balance to be struck and explore alternative possibilities forward.

Over the past decade, the discourse surrounding 'climate crisis' and 'climate emergency' has become increasingly prominent. Stemming from grassroots activism, the use of crisis framing can be seen in radical activist groups like Extinction Rebellion, and the declaration of a climate emergency by New Zealand's Parliament in 2020 [1-2]. However, despite the pressure to use 'crisis framing', studies find that many people harbour doubts over its usage due to the possibility of unintentionally harmful consequences - statements can lack substance or induce anxiety [1]. More broadly, key researchers highlight how crisis framing could be used to reproduce 'status quo' politics and rationalise the overriding of processes and rights, especially those of indigenous communities [1, 3]. Moreover, as the 'climate crisis' becomes a household term, declarations of a 'biodiversity crisis' or 'nature crisis' have cropped up. However, the implications of these have yet to be fully explored. As such, over the summer, we took the first steps to understand crisis framing in New Zealand conservation.

We spoke to ten interviewees from a range of backgrounds, including conservationists, educators, activists, and researchers. Participants were initially identified in our research team's network of contacts and were thereafter expanded using snowball sampling. Interviews were conducted both online and in-person, ranging from thirty minutes to an hour following a semi-structured approach which allowed participants to steer the discussion towards their areas of interest and expertise [4]. The resulting qualitative data then underwent inductive thematic analysis to draw out themes regarding the construction of crisis framing, its motivations, and the subsequent perceived consequences [5]. The following paragraphs explain the initial key themes that we identified throughout this process.

Constructing 'crisis' framing

The purpose of 'crisis' framing as cited by interviewees is to express the realities of biodiversity loss, invoke public action, and gain government funding. Interviewees spoke to the biodiversity crisis primarily in the context of invasive species, habitat loss, and the high proportion of threatened species in New Zealand. Crisis language is then seen as a responsive measure. As explained by one conservationist:

"Some of our species are in real trouble, and you know we're talking about extinction within the next 40-50 years […] so we've got to use that strong emotive language to try and get people to say that this is 'coming or this is happening."

Consequently, crisis language is seen as a necessary tool in the context of government and activist circles:

"Activism and politics/decision-making are places where strong language needs to be used for challenges to be taken seriously. So often facts and science get misunderstood or diluted by politics/big business if the challenges don't fit the agenda of the standing government party/parties."

This particular finding in constructing the 'biodiversity crisis' mimics that found within the 'climate crisis', whereby biodiversity or climate is described as undergoing catastrophe and destruction unless urgent action is taken, leveraging a sense of disaster. The constructed 'crisis' frame can then take on a discursive authority, aligned with the use of scientific language [6-7].

Furthermore, interviewees positioned the biodiversity crisis against other notable crises such as the 'cost of living crisis', 'housing crisis', and 'climate crisis'. To some, the use of crisis framing in the biodiversity context is an attempt to secure government funding and public interest amidst widespread 'crisisification'. This highlights the concept of competing crises. One conservationist expressed that it was easier to justify biodiversity funding under the guise of climate change due to the dominance of the climate crisis label:

"We've had to change our framing in recent years to try and fit with this climate crisis because that seems to be getting more attention and funding."

However, interviewees also stressed that the two crises are inherently interlinked. In this context, crisis language was seen to have some justification. Forest & Bird's utilisation of the term 'dual climate and biodiversity crises', was seen as:

"appropriate given the work of the organisation in activism, lobbying and advocacy."

Our interviewees provide insight into the extension of the crisis framing audience beyond the general public. We note that crisis framing is often directed towards positions of power in an attempt to break their complacency, which highlights emergency framing as a form of responsibility assignment [1].

Disadvantages

However, many also highlight the affective impacts of crisis framing. Examples of this include eco-anxiety among youth, desensitisation, and the counterintuitive effect of diminishing action. On a societal scale, many also pointed to how the 'crisis narrative' can inevitably favour colonial structures of power.

Educators spoke to the realities of eco-anxiety in youth and were conscious about being selective with their choice of language. Speaking to the state of eco-anxiety, an educator recounted:

"It is confronting when, as an environmental educator you hear students as young as eight years expressing their deep concern and hopelessness regarding the state of the environment."

As such, educators expressed concern that crisis framing placed pressure on teachers and prevented student engagement:

"A lot of young students are being exposed to these global challenges in a way which disempowers them as individuals, doesn't connect them with hopeful action and success stories and leaves them with lots of raw emotions and follow-on questions which may not be answered in a hopeful manner."

This excessive usage of crisis language can also desensitise audiences to its emotive impact. As stated in one interview:

"We get used to whatever language is prevalent. So what, are we supposed to keep changing it every 5 years? I just think the focus needs to be on not disempowering and not disengaging people."

Furthermore, expanding upon the concept of competing crises, perhaps a distinctive feature of 'biodiversity crisis framing' is the idea of competing crises within biodiversity itself. The threat classification system that was used to categorise the extinction risk of various species was one of the examples provided in the New Zealand context. Critically threatened species are ranked as the highest priority; however, a high number of species fall into this category and concern was expressed for the overuse of such terminology:

"I don't how you could escalate 'critical' […], but it's hard to use that language when there's so many other crises going on".

Consequently, many interviewees felt that crisis framing could work counterintuitively:

"You can't just continually say 'this is a disaster, this is coming, this is bad' because people will go 'oh, there's nothing I can do'."

Conservationists recounted conversations where sobering language served to alienate some audiences:

"Some people are like, maybe I want to talk about it, but most people who are not in this biodiversity or conservation world shut down, they're like […] you're virtue signalling, you've got an agenda and you're displaying that on your t-shirt, I don't wanna talk about it."

Furthermore, it was noted that conservation had historically been used as a vehicle to override the rights of indigenous peoples - to which crisis language had contributed. Some interviewees were concerned that a crisis framing could continue to produce these dynamics today. Two examples were frequently cited. First, globally and in New Zealand, the creation of national parks and conservation estates has served to confine indigenous peoples and support the confiscation of land [8]. Second, in the New Zealand context, the Wildlife Act legally wrested indigenous ownership of species in favour of crown ownership. As expressed by one interviewee, the dubious historical foundations of conservation are poorly understood today:

"If I went to the Department of Conservation and said to the people 'look the reason why we aren't engaging with you is because you're a symbol of colonisation in place,' they would be like 'No, no we just want to protect nature, like we just want to make sure everything's pristine and that we bring the birds back'. And so there is this disconnect between the history of conservation and the practice of it now."

Crisis framing contributes towards continuing these colonial structures of power through its role in 'securitisation'. To 'securitise' a vulnerability presents it as an existential threat which generates broader endorsement of emergency measures, often by powerful political actors in society. These measures often do not undergo the same rules, consideration, and democratic procedures that would have occurred otherwise [9]. Thus, policies such as the Wildlife Act (implemented by the Crown) are justified under the guise of animal biodiversity conservation, while everything from its inaccurate definition of a 'taonga species' to the barring of indigenous cultural practices regarding eating kererū and kiwi reproduce systems of colonialism that continue today.

Alternative framings and other steps

These critiques are not to say that 'crisis' framing is an inaccurate representation of the situation or that people weaponise the terms purposefully. Rather, what may produce harmful consequences are some of the assumptions that come with the language, and a lack of consideration of wider political implications. To this end, many of our interviewees brought up alternatives to the current 'crisis' framing. Two key examples in particular are mitigating the affective impacts of 'crisis framing' by striking a balance with positive language and action, and engaging with te ao Māori, which expresses an epistemology of urgency differently and advocates for a more personal connection with the environment.

Interviewees stressed the necessity of achieving balance and provided a range of means for doing so. Educators suggested an array of methods, such as sharing success stories and first-hand experiences, and engaging community with hands-on action:

"By showing students the benefits of collective action and giving them the chance to experience action in their own way, we are more likely to have more connected students who value the environment no matter the career path they choose later down the track. Connecting students early on, when they are figuring out their place in the world and in society and how the world could look is important in bringing us closer to our environment as part of a whole system."

Conservationists spoke about working through communities by equipping motivated stakeholders with the tools to inspire others:

"We want to try and use influencers in our communities who have the ear of the politicians. So we talk to these movers and shakers of people and we give them pest control products and we give them restoration advice and they then talk to their local community which includes the politicians."

One of our interviewees highlighted an engaging example of how cultural paradigms and societal values differ in te ao Māori:

"For Māori, [regarding genealogy] it's grandmother, grandfather, and the environment they were in - produced, us... so the rata tree... is an ancestor just as much as my grandmother, my grandfather, my parents. So that's important in terms of whakapapa. And so, when people say, Ko ahau te awa, ko te awa ko ahau, I am the river and the river is me... if it's a part of you drink it... If it's sick, you're sick. The second part is, ... [if] our tupuna put a rahui on a place, and someone breached that rahui, that person was killed. You know, human life was insignificant in this bigger scheme of environmental protection... I don't think you need too much emergency language to say, if people go in and hurt our kereru in here... someone's gonna die; you wouldn't need too much more convincing to follow the rules."
So in this sense:

"If you want to protect the environment, the least you can do is go eat some kererū. Teach your kids how to eat kererū, and kererū is usually a food for women or pregnant women; feed that to your wives and your daughters. Then, I guarantee that once you realise that they're being lost at an alarming rate, you'll want to do something about it."

In engaging with this te ao Māori perspective, the call to responsibility becomes less concentrated on the political agents in power, but rather it comes from the environment itself. Encouraging personal engagement with biodiversity can be an exercise in self-determination for Māori; and for tangata tiriti, it can foster a change in value systems beyond the current individualistic capitalist culture towards one centred in community and environment.

Conclusion

Although 'biodiversity crisis' framing shares many similarities with the 'climate crisis', it can be distinguished in several nuanced ways. While acknowledging its good intentions, participants were concerned that claims of a biodiversity 'crisis' inadvertently cause issues of eco-anxiety, desensitisation, and disillusionment. The crisis label also risks becoming entangled with historically unjust structures of power. This is not to say that crisis framing is useless in communicating the urgency of biodiversity loss; rather, it must be taken with alternatives. Positive language, practical steps, and an engagement with te ao Māori are some ways to reach a discursive parity.

Grace Zhao - **BA (Hons), Sociology**
Grace has completed her Bachelor of Arts degree, majoring in Psychology and Sociology. This year she has enrolled into a Bachelor of Honors degree in Sociology to further explore how our current society is structured to perpetuate systems of power and privilege.

Ethan McCormick - **BA/BSc, Politics & International Relations, Environmental Science, Biological Science**
Ethan is in his final year of a BA/BSc conjoint majoring in Politics & International Relations, Environmental Science, and Biological Science. He is passionate about New Zealand biodiversity and works to support community conservation in the East Auckland area.

Original Research

The Population Genetics of an Avian Alien Invader in Aotearoa: The European Starling (*Sturnus vulgaris*)

Bryan J. Thompson

Population Genetics and Bioinformatics

The factors enabling certain invasive species to adapt and thrive in novel environments remain an unresolved question within the context of invasion biology. An important part of predicting, preventing, or managing biological invasions is understanding which sites of historical introduction were the most successful and why, and which are facilitating ongoing range expansion of these invasive species. Using reduced-representation sequencing data generated from individuals and sourced from five sampling locations across Aotearoa, this study has successfully produced the first high-resolution genomic dataset characterising the population structure and genetic diversity of Common or European starlings *(Sturnus vulgaris)* in their invasive range of Aotearoa.

The Common or European Starling, *Sturnus vulgaris* (hereafter starling), is considered one of the most successful invasive avian species globally, with invasive populations on all human-populated continents [1]. The establishment of invasive starling populations is the result of intentional human-mediated introductions that occurred in the mid to late 19th century [2]. Acclimatisation societies were responsible for the majority of these introductions. These societies were groups specifically formed to introduce plant and animal species across the colonies, aiming to transform these 'new' environments into something more reminiscent of 'home', or to control agricultural or horticultural pests [3]. Unfortunately, in many cases, they were ignorant of the ecological consequences of their actions. Repeated introductions of starlings to multiple locations around Aotearoa occurred between 1862 and 1883 to control insect grain pests, contributing to the present-day invasive population [4].

Successful invasions like those of the starling may appear paradoxical. Despite the often-small size of the introduced population and hence limited genetic diversity to facilitate adaptation, invasive species do not only become established but can flourish under novel environmental conditions. What enables certain invasive species to adapt and thrive in novel environments remains an unresolved question within the context of invasion biology [5].

Many different competing ecological hypotheses exist concerning successful invasives. Examples include the exploitation of vacant niches associated with human activity or the competitive exclusion of native species [5]. An important component of addressing these questions is to understand which historical introduction sites were the most successful and why, and which of these sites are facilitating ongoing invasive range expansion. Genetic data can help to inform an understanding of this invasion history, but despite biological invasions continuing to escalate at an alarming rate, population genomic data are notably lacking for many of the most pervasive and invasive species around the world [6]. Such studies will be crucial to enable evidence-based decision-making if we are to predict, prevent, or manage biological invasions successfully.

We used genome-wide DNA sequencing data to produce the first high-resolution genomic dataset of starlings in Aotearoa to characterise and examine their genetic diversity and population structure. We found a relatively high level of genetic differentiation and population substructuring for samples taken from across the Auckland region, which is congruent with documented introduction histories [7] while also implying restricted gene flow with other regions. Other locations presented with more variable genetic population structure, suggesting potential connectivity between regions south of Auckland. This first insight into the interplay between the biotic and abiotic factors that are shaping invasive starling populations in Aotearoa could potentially inform proactive control strategies.

Methods

Sample Collection, DNA Extraction and Sequencing

106 starling specimen samples were obtained from various sources within Aotearoa from five geographically distinct regions (Figure 1). These consisted of three locations in the North Island: Auckland (AUK: n=18), Palmerston North (PLM: n=12), Upper Hutt (UHT: n=40), and two in the South Island: Blenheim (BLN: n=15) and Canterbury (CAN: n=21). Muscle tissue was subsampled from each individual, and DNA was extracted from these tissue samples and sent to Diversity Arrays Technology Pty Ltd (DArT P/L) for processing and genome-wide sequencing [8]. The DArT method sequences DNA from a random sample of the genome, a method termed 'reduced representation sequencing', to capture a representative snapshot of genome-wide diversity.

Data Processing, Mapping, Variant Calling and Filtering

Once we received the raw DNA sequence outputs from DArT, a series of software programs and pipelines were used to process these raw outputs. We identified a list of variable sites in the genome where there was a single DNA base change within a sequence (single nucleotide polymorphisms, or 'SNPs'). SNPs capture diversity between individuals and between sampling locations, and SNP variants can be used to cluster individuals by their similarity and determine which sampling sites are genetically dissimilar to each other. In brief,
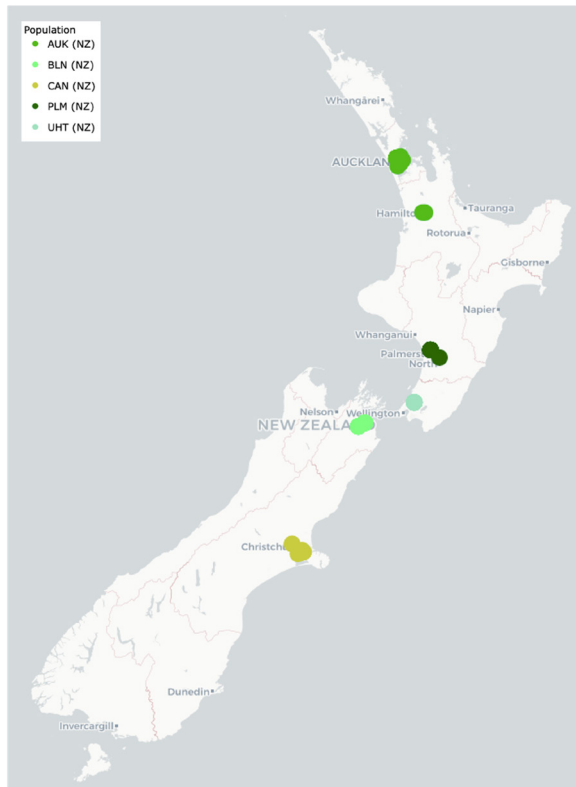
Figure 1: Map showing starling locations sampled across the Aotearoa invasive range. Site abbreviations: AUK - Auckland, PLM – Palmerston North, UHT – Upper Hutt, BLN – Blenheim, CAN – Canterbury.

we used Fastp v0.23.2 [9] to trim DNA sequence lengths to 70 bases and discard all sequences shorter than 40 bases. We used the Stacks v2.2 [10] pipeline to discard low-quality sequences, remove sequences with uncalled bases, and also remove the restriction enzyme recognition sites (Pstl & Sphl). Next, we used BWA v0.7.17 [11] to index our reference genome S. vulgaris vAU1.0 [12], align the sequences, and produce output files containing the alignments and their respective base qualities. Alignments were sorted and indexed using SAMtools v1.16.1 [13], and SNPs were called and annotated using BCFtools v1.16 [14]. We then systematically removed replicates and siblings from the dataset using DartR v2.9.7 [15], resulting in a final individual count of 76 (N=76). Finally, we used VCFtools v0.1.15 [16] to filter out poor-quality SNPs and remove SNPs present in less than 50% of the individuals in each sampling location. We ran one final filtering step to ensure low levels of missing data (due to technical errors during sequencing or issues sequencing particular segments of DNA), resulting in a final dataset containing 29,117 unique SNP sites.

Analysis

The SNP dataset was analysed to extrapolate Aotearoa population structuring and spatial partitioning. R v4.2.1 [17] was used with the Bioconductor and DartR suite of packages to generate principal components analysis (PCA), which can be used to visualise how genetically similar populations are based on how much they overlap or how closely they cluster together on the plot. DartR was used to calculate a metric of pairwise population differentiation (pairwise FST) between sampling locations and to report SNP variants that were only found in one site ('private alleles') by comparing each sample location against the aggregation of all other locations (method = one2rest). Finally, Admixture v1.3.0 [18] was used to infer ancestry proportions, with individuals sharing similar ancestry profiles if they are genetically similar.

Results

Population Structure of Aotearoa Starlings

Our PCA of the five Aotearoa sampling locations reveals varying degrees of subpopulation structure within Aotearoa, with the exception of Palmerston North (PLM) and Upper Hutt (UHT), which form a single cluster of genetically similar individuals (Figure 2). Auckland (AUK) is the most divergent of the Aotearoa sample locations on PC1, with the greatest differentiation existing between Blenheim (BLN) and AUK. This level of population differentiation is supported by the corresponding pairwise FST value between these two locations (FST = 0.043; higher values reflect higher levels of genetic difference between populations) (Figure 3). Except for AUK, pairwise FST values for all Aotearoa locations fall in the range of 0.007 to 0.016, while AUK pairwise FST values are notably higher, falling in the range of 0.031 to 0.043 (Figure 3). When we plotted ancestry admixture with the assumption of two distinct starling lineages, our findings supported this pattern. The distinctive clustering of AUK compared to all other sampling locations and the differentiation between AUK and BLN matched our admixture assumptions. (Figure 4).

Of the genetic diversity indices we examined, of note was the relatively high number of private alleles (113 private alleles) for AUK (Table 1). Additionally, both PLM and UHT have a relatively low number of private alleles (PLM = 2, UHT = 0) relative to the other sampling locations.

Discussion

Using reduced-representation sequencing data generated from individuals sourced across five sampling locations in Aotearoa, this study has successfully produced the first high-resolution genomic dataset characterising the population structure and genetic diversity of starlings in the invasive Aotearoa range.

#### Genetics and Introduction History of Starlings in Aotearoa

As documented in shipping records and records from acclimatisation societies, starlings were introduced to Aotearoa between 1860 and 1873 in multiple shipments to primarily three locations: Auckland, Canterbury, and Otago, with the majority of introductions in other regions reportedly resulting from translocations from the established Otago population [4]. Our data displays a pattern in the genetic population structure congruent with this introduction history regarding Auckland, but less of a match with the introduction history of Otago and
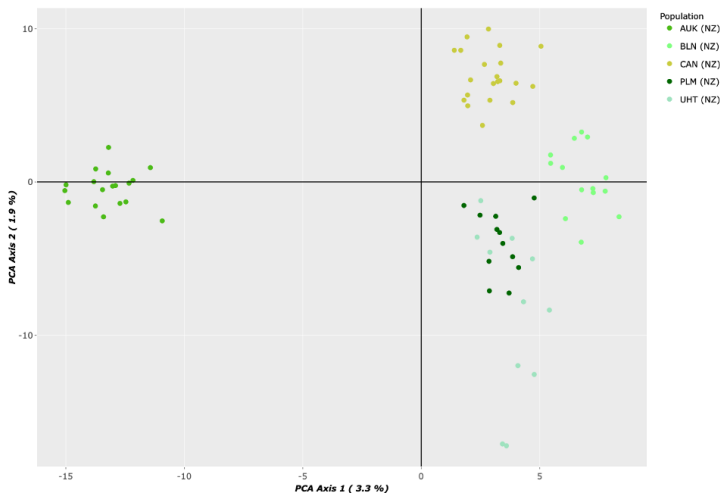
Figure 2: PCA of the genetic data from five sampled locations from the Aotearoa invasive range. Each dot represents an individual starling and their genetic data. The plot displays PCA axis 1 (3.3% variance explained) and PCA axis 2 (1.9% variance explained) and illustrates that Auckland (AUK) is genetically distinct from other sampling locations.
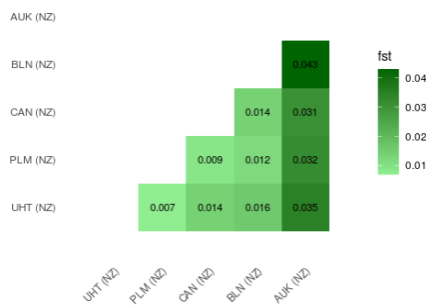
Figure 3: Heatmap of pairwise analysis of the genetic differences (measured as pairwise FST) between each of the five sampled Aotearoa invasive range locations. Brighter green indicates a higher FST, which indicates more genetic differentiation. The highest genetic differences are between Auckland and all other locations.
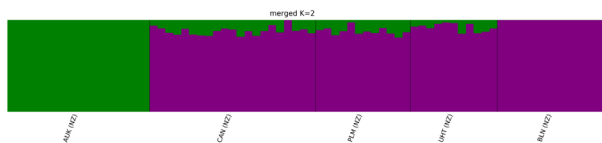
Figure 4: Admixture ancestry profile of Aotearoa sampling locations assuming two distinct ancestral source populations. Each vertical bar represents an individual, and the proportion of the two ancestries (green versus purple) are shown. Most individuals are overwhelmingly one colour, indicating they are of a single ancestry with little mixture between the source populations.

Sample Locations	N	Private Alleles
AUK (NZ)	18	113
BLN (NZ)	14	23
CAN (NZ)	21	38
PLM (NZ)	12	2
UHT (NZ)	11	0

Table 1: Consolidated table showing the sample sizes (n) for the five sample sites, and the number of private alleles for each location. Large numbers of private alleles indicate genetic distinctiveness compared to other locations.

Canterbury. Notably, although we have sampled Canterbury directly, we are limited to inferring the Otago population indirectly from the Blenheim, Upper Hutt, and Palmerston North samples. These locations reportedly received the majority of their stock from Otago translocations.

In addition to the observed genetic differentiation and distinctive admixture evident in starling ancestry, Auckland's introduction history is further supported by the relatively large number of private alleles compared to the other Aotearoa sampling locations (Table 1). Private alleles in other invasive species have been attributed to introductions from different source locations [19]. The retention of these private alleles in Auckland also suggests that gene flow is likely restricted between Auckland and the other Aotearoa sampling locations. This restriction implies that it may be possible to manage starling populations in the Auckland region in order to control the negative impacts that starlings are having, particularly at vineyards in the region.

While a distinct signal of introduction history and restricted gene flow is evident in Auckland, it is not as clear for the remaining sample locations. There may be a degree of connectivity and gene flow between these southern locations. Parts of the South Island of Aotearoa experience winter temperature conditions at the lower end of starlings' thermal tolerance [20], which could trigger some northward dispersal. Of particular note is the lack of genetic differentiation between Canterbury and Palmerston North (pairwise Fst 0.009), two locations that were reportedly founded from different sources [4]. Individuals may travel between these locations, perhaps via seasonal migration. Except for Auckland, these two sampling locations span the largest geographical distance, with Blenheim and Upper Hutt located between them (Figure 1).

Conclusion

In summary, our study has demonstrated that demographic effects associated with the dynamics of introduction history strongly influence genetic diversity and contemporary population structure for starlings in Aotearoa. Furthermore, we have uncovered variable levels of spatial partitioning across the invasive Aotearoa range suggesting that dispersal, and subsequently gene flow, may be restricted in some but not all sampling locations. This provides some evidence that local species management programs may be successful in reducing the numbers of this invasive pest in Aotearoa.

Acknowledgments

First, I want to acknowledge my supervisor, Dr Kat Stuart. Kat's unwavering patience and exceptional knowledge of computing and genetics meant I got so much more out of this scholarship than I ever thought possible. I also want to thank Associate Professor Anna Santure for her constant support and encouragement - I wouldn't have taken up the offer without it. Finally, I want to thank everyone in the Santure Lab. They are an incredibly talented group of computational biologists and great people who make it a fun and relaxed environment to work in.

Bryan J. Thompson - BSc, Biological Sciences (Evolution) and Anthropological Science

Bryan is in his final year of his BSc, double majoring in Biology and Anthropological Science. He is interested in the interplay between proximate and ultimate mechanisms of evolution and how they together shape species over time. He plans to start his MSc in 2025.

Original Research

Examining Textural and Compositional Variations of Hot Spring Deposits to Understand Trace Element Biosignatures in Relation to Early Life on Earth and Mars

Dominique Stallard

Geology and Astrobiology

Investigating the textural and compositional variations of siliceous hot spring deposits, along with their trace element biosignatures, is vital. These microbial and paleoenvironmental textures are important to research as they could be related to the beginnings of early life on Earth and possibly ancient life on Mars.

This summer, I had the opportunity to join Associate Professor Michael Rowe and Professor Kathy Campbell in researching the textural and compositional variations of siliceous hot spring deposits. Research on these materials, also known as sinter, is vital when investigating the trace element biosignatures that could be related to the beginnings of life on Earth and possibly Mars. My research seeks to address the viability of chemical biosignatures by combining petrography, rock composition, properties of thin sections of sinter rocks using optical microscopy, and chemical mapping of microbial textures preserved in hot spring materials from around New Zealand. Overall, I am investigating paleoenvironmentally significant textures at a fine scale.

Hydrothermal silica deposited in hot springs (sinter) is known to harbour thermophilic (heat-loving) microbes that can survive in extremely harsh conditions. These microbes are integral to studying the development of primitive life forms in Earth's history. As early conditions on Earth are thought to have been hotter and harsher, similar to other planets in our inner solar system, these terrestrial examples may potentially provide insight into the development of ancient life on Mars billions of years ago, around the same time as it took place on Earth. The build-up of a sinter deposit is related primarily to the precipitation of hydrothermal silica [1]. Moreover, silica deposits, specifically water-bearing opaline silica, thought to have formed through mechanisms similar to those in hot spring environments on Earth, have been identified on Mars. These deposits likely formed in hot springs active on the Martian surface more than 3.6 billion years ago [2], [3], providing a compelling target in the search for life elsewhere in the solar system.
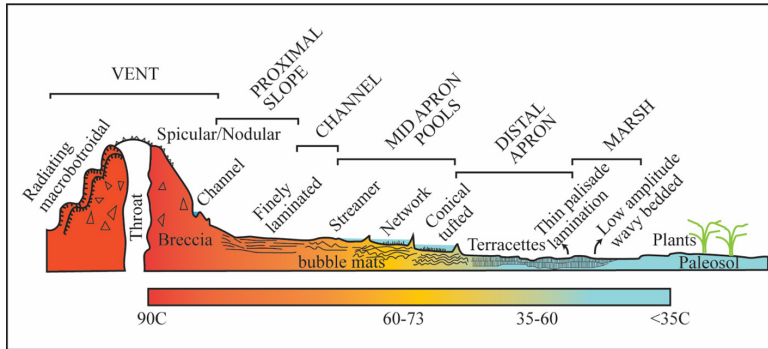
On Earth, sinter forms in geothermal areas like Rotorua at different temperatures, from high-temperature vents (>75-100°C) at the spring source to cool, geothermally fed marshes (~25°C) [4], [5]. This influences macroscopic and microscopic textures, such as microbial growth patterns, as microorganisms living in the hot spring waters become trapped within the developing sinter rock deposit. These conditions often fluctuate, affecting the growth rate and patterns of thermophilic microbes due to the changes in fluid flow rate, temperature, and pH of the hot spring over time. The challenge here is that organic material fossilised in the sinter breaks down over time. This means that many of the indicators used to identify biosignatures are no longer preserved after billions of years in rocks that may preserve some of the earliest life forms in ancient hot springs [1]. Therefore, it is important to look at new ways of identifying evidence of biological processes. In this project, I examined microbial textures in

sinter forming under varying spring discharge fluid conditions. I correlated this with chemical mapping of the same material to identify how widespread inorganic chemical signatures of biological processes (biosignatures) may remain in the sinter rock long after the organic material of thermophilic microbes has decayed away.

Methods

This study utilised 17 samples of hot spring sinter, mostly from New Zealand, representing a range of different environmental conditions. Representative materials from each sample were prepared for optical microscope examination. The sinter rock materials were cut and polished down to only 30 micrometres thick so that light could pass through the wafer-thin rock. This allowed for petrographic observation of textural relationships between the fossilised microbes and plants that were living in the geothermal waters and the silica precipitate that entombed the organisms in the developing sinter deposit. Petrographically, the textures and features observed under the microscope are linked to the growth of thermophilic microorganisms and relate definitively to the sample's location along the vent-to-marsh thermal gradient. This therefore tells us about the specific environmental conditions under which the rock formed (Figure 1). Such variable paleoenvironmental conditions affected the growth of hot spring-related microbial life, representative trace elemental biosignatures, and the types of patterns/textures entombed and preserved in the sinter. Characterising these textures and growth patterns is important in understanding how these microbes have been able to flourish in harsh conditions. In addition, all samples had previously been chemically mapped at the Institute for Planetary Materials,

Okayama University on an electron microprobe, providing two-dimensional images of the chemical variability in each sample. Electron probe microanalysis (EPMA) measures the concentrations of major elements, which in this case are associated with both microbial life and environmental processes. Elemental concentrations around and within silicified microbial filaments are often well preserved, detailing growth patterns. This research project required processing the EPMA images and comparing them to textural observations from the microscopy I undertook.

Figure 2: Comparison of the EPMA and petrographic imagery of a palisade texture sample. Aluminium is observed to be primarily concentrated around "sheaths" of the course filament laminations and terracettes. These filaments fluctuate in length but are largely uniform, indicative of low-temperature conditions (calothrix/cyanobacteria growth).

Figure 1: Diagram of the schematic cross section of a hot spring/geothermal paleoenvironment [4] with temperature gradients [5], highlighting the differing microbial textures developed across the apron.

Conclusion

Textures, both macroscopic and microscopic, suggest sinter samples in this research likely precipitate from fluids with a temperature range of <40-90°C and mostly from alkali-chloride near-neutral pH thermal waters. These types of thermal fluids characteristically construct large sinter aprons, as observed at Orakei Korako or Wai-O-Tapu, for example. I observed variations in the orientation of silicified microbes through individual samples, with some growing parallel to the flow of thermal water down a hot spring discharge channel, while others grew vertically in shallow hot spring pools. The filaments also varied in thickness, ranging from a few micrometres to over 10 micrometres. Silicified plant material was also present, with some samples having abundant reed and marshy material, along with algal balls and diatoms representing a range of different types of "life".

Textural evidence of microbes varied depending on their proximity to the vent, forming unique microbially mediated textures within hot spring "sub-environments", related to their distance from the ancient spring-vent discharge point. Within these textures, there were clear variations in density, thickness, and growth habits of the microbial fossils in the silica, reflecting the type and abundance of microbial/organic material within each sample. Microbial filaments, one of the most common and easily identifiable microbial textures, are interpreted to be fossil cyanobacteria (photosynthesising bacteria), typical of medium to low sinter apron discharge temperatures (Figure 2). The orientation of filaments is indicative of changing fluid flow direction and microbial growth, while the size of the filaments relates to the temperature and water depth during silicification.
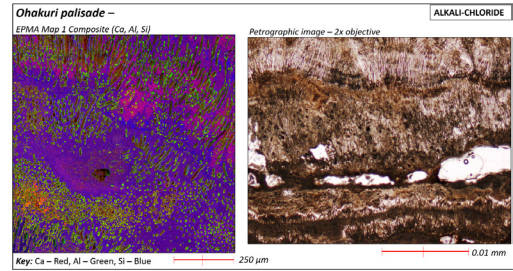
Geochemically, it is clear that the high-temperature sinter textures have distinctive characteristics. Sinter from the vent region has dense silica with minor instances of calcium and aluminium in the layers and no clearly identifiable microbes at the rather coarse resolution of optical microscopy. However, it is evident from other studies that these textures are constructed of very finely layered microscopic organic biofilms (Figure 3). In contrast, the microbial filaments evaluated in this study, within the lower temperature domains, are characterised by strong chemical enrichments in aluminium, and sometimes calcium, which are isolated in discrete zones around the filaments. These zones are interpreted to represent the outer "sheath" of the microbe which has been silicified. A recently completed MSc thesis from the University of Auckland [2], focusing on a specific morphology of sinter deposit, also highlights the concentrations of metals in relation to cyanobacteria filament morphology. In both Nersezova's study [2] and this research, there is a clear sentiment that these "sheaths", with their durable preservation potential and specific elemental chemical enrichments, may be the best biosignatures to focus on when endeavouring to understand early life in hydrothermal paleoenvironments on Earth and possibly Mars. However, results also suggest that these particular biosignatures may be unique to cyanobacteria; will other microbial species show similar traits?
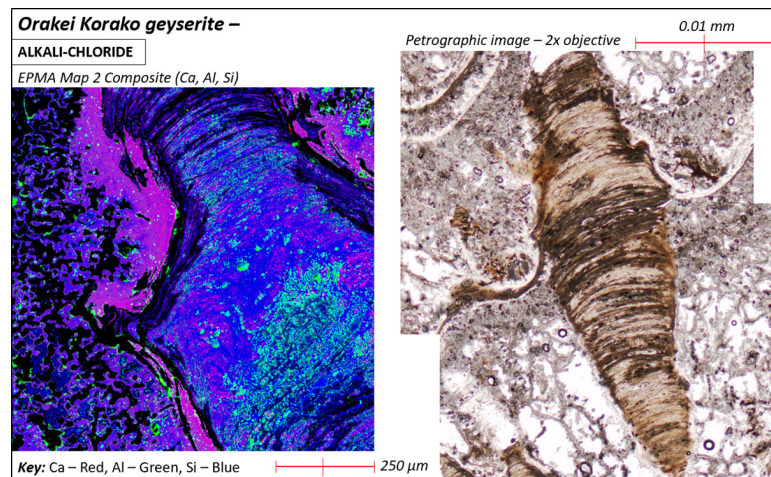
Figure 3: Comparison of the EPMA and petrographic imagery of a geyserite texture sample. High concentration of silicon is observed throughout the spicule structure with instances of aluminium and calcium, although no definitive microbes. The spicule has a fluctuating density of organic layers with lateral linkages to the surrounding fabric.

Takeaways

· The strongest chemical signature of biological activity is observed around filaments in the low-temperature siliceous hot spring deposits, or sinter.
· High-temperature sinter, which forms close to the vent, has less definitive chemical biosignatures due to difficulties in imaging features at a very fine scale using the methods of this study.
· When exposed to acidic conditions, many of the biosignatures are altered and less apparent.

· This research supports the findings of the previous MSc thesis from the University of Auckland [2], which focused on one particular sinter morphology and found distinct chemical biosignatures physically associated with microbial filaments.

Acknowledgments

Dominique Stallard - BSc, Earth Science
Dominique is graduating in September with a BSc in Earth Science and will pursue an Honours year, during which she will continue to study these siliceous hot spring deposits. She has developed a passionate interest in astrobiology and finding life on Mars, and is excited to research in this field.

Original Research

Large Eagles, Even Larger Data: Methods for Handling Large Satellite Datasets for Monitoring Eagle Movement in Europe

Adele Gao

Geographical Information System and Data Processing

Big data is common in geographical research, most of which is spread across different locations and times. It is usual for researchers to take days, even months, to complete basic calculations for those data. For the torrent of movement points—over 35 million—collected by the British Trust for Ornithology, is there a better way to see how 'wet' areas near the movement paths of Greater Spotted Eagles are?

The Polesia region in Eastern Europe is the stronghold for the Greater Spotted Eagle population. According to Project Polesia - Wilderness Without Borders, the region is home to more than 16% of Europe's endangered species, with the eagle being a totemic example that has both ecological and cultural importance [1]. This project is focused on supporting a research effort into how eagles in the Polesia region change their behaviour based on environmental differences in the wetlands. In other words, how 'wet' is the landscape surrounding the movement points of eagles?

The British Trust for Ornithology gathered eagle movement data, and we have used Google Earth Engine to assess the normalised difference water index (NDWI) around the movement points. Satellite data is the only viable way to monitor the environmental conditions due to Russia's invasion of Ukraine. The Polesian region is located half in Ukraine and half in Belarussian territory - incorporating the Chernobyl exclusion zone. The combination of war and radioactive contamination means that remote sensing is a vital tool in monitoring the affected ecosystems.

We calculated the NDWI for daily areas of interest (AOI) generated from the

Glossary

Normalised Difference Water Index (NDWI) are remote sensing-derived indexes related to liquid water. For this research, we used the NDWI to detect water bodies alongside the eagles' movement points. For the Sentinel-2-based calculation, we used "Green" Band 3 and "Near Infrared (NIR)" Band 8 [2]. For the MODIS-based calculation, we used "Near Infrared (NIR)" Band 2 and "Shortwave Infrared (SWIR)" Band 6 [3].

Formula for Sentinel-2-based calculation:
NDWI = (Band 3 - Band 8)/(Band 3 + Band 8)

Formula for MODIS-based calculation:
NDWI = (Band 2 - Band 6)/(Band 2 + Band 6)

Sentinel-2 is a constellation of two identical satellites in the same orbit, imaging land and coastal areas at high spatial resolutions (10 m, 20 m, or 60 m) in the optical domain. [4]. The revisit frequency of each single Sentinel-2 satellite is 10 days, and the combined constellation revisit is 5 days [2].

Moderate Resolution Imaging Spectroradiometer (MODIS) is a key instrument aboard the Terra and Aqua satellites. Terra MODIS and Aqua MODIS view the Earth's entire surface every 1 to 2 days, acquiring data in 36 spectral bands or groups of wavelengths [5].

Visual representation for NDWI values of Area of Interest and movement points
(Date : 2019-10-02)

Legends

Daily Area of Interest
Sentinel-2 based NDWI value:-0.3048
MODIS based NDWI value: 0.1090

NDWI value for movement points (MODIS)
- 0.036 - 0.047
- 0.047 - 0.064
- 0.064 - 0.11
- 0.11 - 0.16
- 0.16 - 0.243

NDWI value for movement points (Sentinel-2)
- -0.523 - -0.314
- -0.314 - -0.184
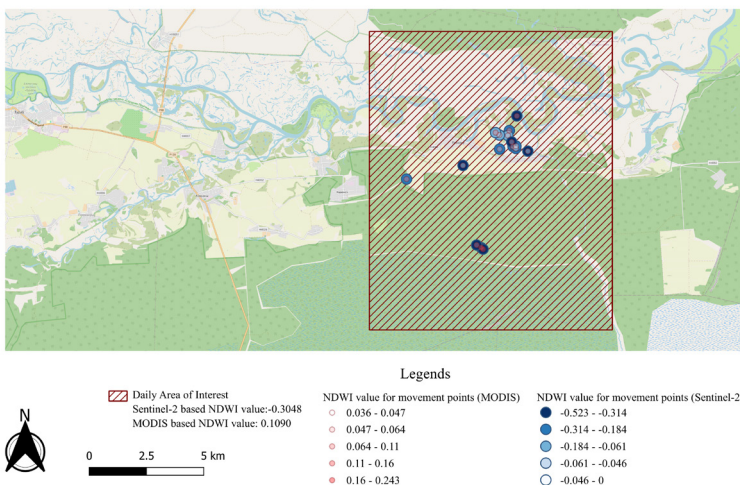- -0.184 - -0.061
- -0.061 - -0.046
- -0.046 - 0

Figure 1: Map of the study region, including eagle movement points and area of interest with NDWI values. Example data refers to movement points from October 2, 2019. Image by Adele Gao using QGIS.

coordinates from the movement data based on dates. We also calculated the sample movement points that were collected between October 1 and October 2, 2019 in order to examine some of the issues around the data handling in more detail. The movement information as a whole is a huge dataset of 35 million points that presents significant challenges in extracting the environmental parameters from the satellite data record. Our work therefore seeks to enable chronological and geographical comparisons of the NDWI values that could then be used to monitor the change in wetlands across the region.

Method

Charlie Russell and Dr Adham Ashton-Butt from the British Trust for Ornithology provided the movement data used in this work. The raw data contains 35,610,268 points across the Polesia region from 2018 to 2022. These 35 million data points are the core of the problem faced. How can we process them in an effective manner,
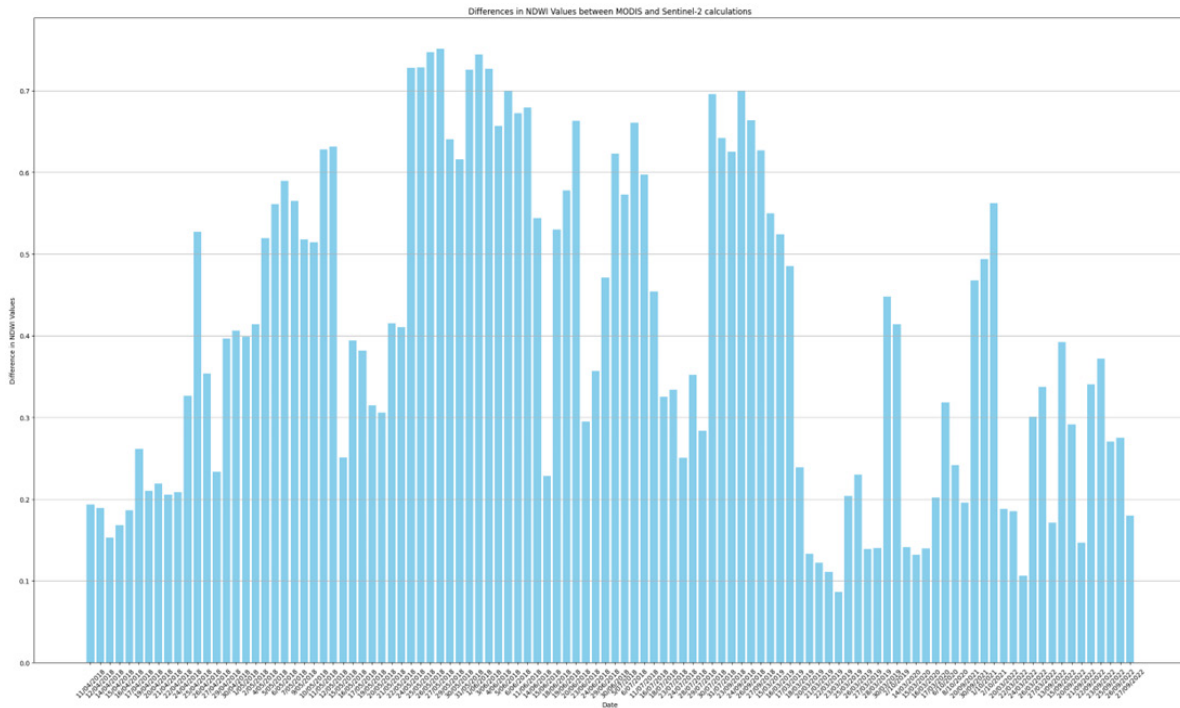
Figure 2: Graphic representation of differences between NDWI for daily AOI calculated based on Sentinel-2 and MODIS (NDWI_MODIS − NDWI_Sentinel-2 = Differences in values). Image by Adele Gao in Google Colab.
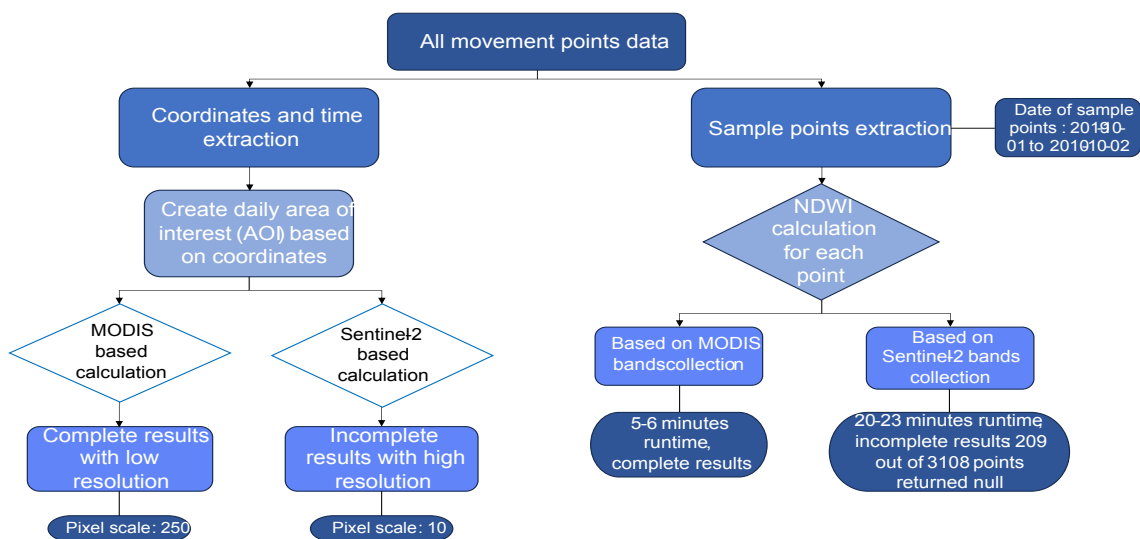
Figure 3: Flow chart of NDWI calculation. Image by Adele Gao using Microsoft PowerPoint.

whilst also managing the tera-bytes of satellite data that will be providing the contextual environmental information?

Data Pre-processing
We wanted to compare the NDWI values to study wetland changes chronologically. Therefore, we sorted the movement points based on their recording time using functions from the Pandas library. We then filtered through the grouped data for each day's maximum and minimum latitude and longitude. The new data frame calculated the daily NDWI based on the AOI created with the daily maximum and minimum latitude and longitude as coordinates. It is this step that enables us to batch process the movement data record through the Google Earth Engine API on a daily basis, whilst remaining under the spatial extent quota.

Calculation of NDWI for daily AOIs
The calculations used Band 3 and 8 from the Sentinel-2 collection with a pixel scale of 10 m. It took nine minutes to finish the calculation for the 963 daily AOIs. This compares to it taking three months if we were to process each (35 million) point one by one through the earth engine API. We also used Band 1 and 2 from MODIS with a pixel scale of 250 m. It took 12 minutes to finish the calculation for the 963 daily AOIs.

The same AOI had different NDWI values from the calculations based on the two different datasets. The difference between the two results were less than 0.8, and the pixel scale difference between the MODIS and Sentinel-2 bands collection was around 200-230 m for this calculation. The pixel scale drives the difference in observed values as the contents of each pixel is fundamentally different between the sensors.

Calculation of NDWI for each point
For comparison, we calculated the NDWI for each movement point in our October subset. We extracted 3,108 movement points from October 1 to October 2, 2019. The calculation using Sentinel-2 data (Bands 3 and 8 with a pixel scale of 10 m) had a runtime of 20-23 minutes for each of the 3,108 points. The results were incomplete, with 209 points returning null. The MODIS calculation used Bands 1 and 2 with a pixel scale of 250 m to calculate the NDWI for the 3,108 points. Each point returned a valid NDWI value, and each point's runtime was 5-6 minutes. Therefore, the daily AOI approach is the preferred method moving forward.

Discussion

Data availability
Due to the long revisit time of the Sentinel-2 satellites, most of the results returned from the calculation for daily AOIs were null. In contrast, calculations based on MODIS returned complete results for all 963 AOIs due to the daily revisit time of the Terra and Aqua satellites on which MODIS is mounted. However, due to the large pixel scale for MODIS calculations, the results are very different from those based on Sentinel-2, with a difference of 0.8 between the two.

To improve this, we could use combined results and estimate more accurate NDWI values based on the differences between the two sets of calculations. Another plausible approach would be calculating the margin of difference between the two result sets and making estimations for Sentinel-2 results based on such differences. Alternatively, we could use another set of satellite data, for example, Landsat collections, to compare with MODIS and Sentinel-2. However, the results were also incomplete based on test calculations done from the Landsat collection.

For the point NDWI calculation, we chose a small part of the whole set of movement points as sample data based on the availability of daily NDWI results; October 1 to October 2, 2019, returned valid NDWI values when calculated based on their AOI. Sentinel-2 data can return valid results for most movement points. Therefore, we could use the results based on MODIS as a background reference for the final NDWI values.

Further work
So far, we have only calculated NDWI as the indication for wetness; there are other factors to be considered in the context of the Polesia region, such as soil moisture and precipitation for the AOIs, which could be gained from a range of other sensors. Further work is required to develop these data streams and integrate them into the time-AOI batch processing approach.

Since evaluating the relationship between the eagle movement and wetness of the environment required more than one environmental measurement, we are unable to draw conclusive findings on correlation between eagle movements and the environment. However, the method for calculating the NDWI is a step forward in simplifying the analysis for big data and can be implemented to other geographical data processing.

Conclusion

Using the cloud processing abilities of Google Earth Engine, we were able to extract and calculate an environmental parameter from a large satellite data record, in a fraction of the time it would have taken with a point-by-point approach. The British Trust for Ornithology now wants to take this approach and apply it to their other wildlife monitoring programmes, expanding on the range of sensors and parameters used to truly monitor the wetland conditions as experienced by the animals living within them. Given the on-going war in Ukraine, this remains the only way to monitor how vulnerable species are coping with both the impact of the war itself and our changing climate.

Acknowledgements

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Adele is a fourth-year science student majoring in geographical information science (GIS), focusing on GIS-oriented programming and spatial analysis. She is interested in environmental development, animal geography, and GIS application in urban areas. Outside of study, she enjoys playing video games, her favourite being the Fallout series.

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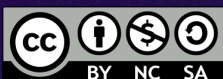
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