The role of the sympathetic nervous system in multiple myeloma progression

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Introduction

Multiple myeloma (MM), which is the second most common hematologic malignancy in the United States, is an incurable malignancy of bone marrow plasma cells. MM is always preceded by a common asymptomatic state known as monoclonal gammopathy of undetermined significance (MGUS). Despite the genetic similarity between MGUS and MM, progression only occurs at a rate of 1-2% per year (Kyle, 2002). This low progression rate suggests that non-genetic factors play a significant role in the development of MM.

One such non-genetic factor could be chronic intermittent hypoxia (CIH), a key component of sleep apnea. Figure 1 shows that, when compared to normoxia-exposed C57BL/6J mice, which are usually resistant to MM, CIH-exposed C57BL/6J mice were more vulnerable to MM cells, with 67% of the mice developing terminal paralysis (Ali, 2019). This correlation may be explained by the increase in sympathetic tone caused by CIH, but no studies have been conducted on this matter. The first step to conducting such a study, however, would be to prove that the sympathetic nervous system can be inhibited.

Methodology

To establish a baseline with which to compare sympathetic responses, we measured 4 male and 2 female mice’s response to dobutamine, an agent which mimics epinephrine. We then supplemented the mice’s regular chow and water with Nutri-Cal and 0.25% saccharine water as well as a 0.001 mg/mL propranolol solution to their Nutri-Cal. We then supplemented the mice’s regular chow and water with Nutri-Cal and 0.25% saccharine water and measured the mice’s average food and water intake. With that information, we dosed 9 animals with 100 mg/kg/day of propranolol by adding 5 mg/mL of propranolol to their saccharine water as well as a 0.001 mg/mL propranolol solution to their Nutri-Cal. We then placed 6 of the dosed mice in the CIH chamber and the other 3 in the normoxia chamber. We also placed 3 undosed animals in the CIH chamber and 3 in the normoxia chamber to serve as a control. After several days, we measured the mice’s baseline heart rate and challenged the mice with dobutamine to test whether the dosed mice were beta-blocked.

Results

Heart Rate

<table>
<thead>
<tr>
<th>Condition</th>
<th>Heart Rate (bpm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CIH</td>
<td>700</td>
</tr>
<tr>
<td>Normoxia</td>
<td>600</td>
</tr>
<tr>
<td>CIH + Propranolol</td>
<td>400</td>
</tr>
<tr>
<td>Normoxia + Propranolol</td>
<td>300</td>
</tr>
</tbody>
</table>

Figure 3: Baseline heart rate data without addition of dobutamine demonstrating mice dosed with propranolol have lower baseline heart rates as compared to those of the mice that were not given propranolol.

Dobutamine Challenge

<table>
<thead>
<tr>
<th>Condition</th>
<th>Heart Rate (bpm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CIH and Propranolol</td>
<td>900</td>
</tr>
<tr>
<td>Normoxia and Propranolol</td>
<td>800</td>
</tr>
<tr>
<td>CIH</td>
<td>700</td>
</tr>
<tr>
<td>Normoxia</td>
<td>600</td>
</tr>
</tbody>
</table>

Figure 5: Response of mice exposed to CIH and dosed with propranolol
Figure 6: Response of mice exposed to CIH but not dosed with propranolol
Figure 7: Response of mice in normal oxygen conditions and dosed with propranolol
Figure 8: Response of mice in normal oxygen conditions but not dosed with propranolol

Implications

Modern cancer drugs pose staggering financial burdens. State-of-the-art treatment for newly diagnosed myeloma requires regimes that are unaffordable for even well-insured patients. At an average of $100,000 per year for a new cancer drug, many myeloma patients will not receive the medicine (Tomasson, 2018). An understanding of how MGUS progresses to MM would allow for the identification of those at highest risk of MM and the development of more cost-efficient and effective treatment and prevention plans. Our study has taken the first step to achieving this understanding by showing that CIH elevates sympathetic tone and that it is possible to inhibit this increase in sympathetic tone with beta-blockers. Essentially, our study has begun to investigate the role of the sympathetic nervous system in the progression of MGUS to MM. Future studies should focus on the relationship between increased sympathetic tone and malignant cell engraftment as well as the specific effect the sympathetic nervous system has on the bone marrow microenvironment.

Acknowledgements

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References


Enabling User-Defined Security Policies for Programmable IoT Systems

Samuel Berkun, Dr. Omar Chowdhury, Moosa Yahyazadeh

Introduction

- People use Internet of Things (IoT) systems to control their smart devices, in their smart homes
- IoT platforms rely on downloading third-party apps, which may be malicious
- PATRIOT (Policy Assisted Resiliency for IoT automated systems) ensures safety by filtering action requests in IoT systems

About PATRIOT Framework

- When applications want to control devices, they send action requests to the IoT platform. For example, an app might send a request that says “Open the bedroom window”.
- PATRIOT runs on the IoT platform, where it controls the flow of requests. For each request, PATRIOT either allows or denies the request. This decision is based on the security policies defined by the user.
- Users can define policies directly in the language, or use the Graphical User Interface (GUI) to automatically generate them.

Language and GUI Design

- Since PATRIOT is meant to be usable by everyone, language and GUI are designed to be as simple and intuitive as possible
- Language is high-level (close to English) and meant to translate from intuitive user expectations
- GUI consists primarily of selection menus, to make it impossible to create invalid syntax
- GUI developed as a web interface using HTML/CSS and Bootstrap framework
  - available for any device with a web browser

Acknowledgments

I am grateful to everyone in the Computational Logic Center at the University of Iowa for welcoming me to their lab. I would like to thank Dr. Omar Chowdhury and Moosa Yahyazadeh for bringing me onto the project, as well as taking the time to explain everything to me and making sure I was comfortable with my work. Finally, I would like to thank the Belin-Blank Center for providing me this opportunity.

Traces and Policy Analysis

- Conditions in the PATRIOT language can have temporal formulas - essentially, filtering depends on past events as well as present
- PATRIOT treats the past as a sequence of states, which is called a trace. A state is stored whenever an action occurs. See Figure 3 for an example.
- Occasionally, it may be possible for the system to reach a point where it gets stuck: The policies are defined such that with the current trace, no actions are allowed.
- The PATRIOT policy analysis warns the user if the user-defined policies may cause the system to get stuck in the future
- Analysis is done by converting policies into SMT formulas, which are processed by the Z3 SMT solver.

SMT Solving

- SMT solvers, such as Z3, check whether a set of first-order logic formulas are satisfiable. See Figure 5 for an example of this.
- Each policy is essentially a formula of the form “action implies condition”

Conclusions and Future Work

- Use of PATRIOT language structured policies allows avoiding many issues with previous implementations
- Analysis can be expanded and improved in efficiency: Alternate definitions of “stuck” trace
- Adoption of system into smart home platforms; improving usability

References


Elucidating the role of angiopoietin-like protein 5 in plasma triglyceride metabolism

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Medical Implications
- Fatty acids not used for immediate calories are stored as triglycerides; some circulate in the bloodstream
- Elevated plasma triglyceride levels leads to the formation of atherosclerotic plaques (Pruthi et al., 2018)
- Results in cardiovascular diseases (heart disease and stroke)

Objective: To determine the role of ANGPTL5 in LPL inhibition and plasma triglyceride metabolism.

Results: Fluorescent Immunodetection of ANGPTL5

Preliminary Western Blots of ANGPTL5

LPL Activity Assay

Secondary Western Blots of ANGPTL5-8

Co-transfected LPL Activity

Co-transfected LPL Activity

LPL Activity Assay

Figure 1: ANGPTL3-8 form a complex to inhibit LPL and increase plasma triglycerides

Figure 2: LPL cleaves the quencher off of EnzChek triglycerides to produce measurable fluorescence

Conclusions/Implications
1. ANGPTL5 has no significant effect on LPL activity
2. ANGPTL5, in complex with ANGPTL8, does not inhibit LPL; may enhance ANGPTL8 secretion
3. ANGPTL5 is not secreted effectively

Development of Atherosclerotic Therapeutics
- By determining how ANGPTL5 is involved in triglyceride metabolism, cardiovascular therapeutics become plausible.

Future Directions
Aim 1: Perform endothelial lipase inhibition assays with ANGPTL5
Aim 2: Co-transfect with ANGPTL4 (and other family members) to determine if ANGPTL5 counteracts inhibitory effects

Experimental Design

Acknowledgements
Special thanks to Shwetha Shetty and Dr. Davies, the Belin Blank Center, and the Department of Biochemistry of Carver College of Medicine for their guidance and resources during this project.

References

Figure 1

Figure 2

Figure 3

Figure 4

Figure 5

Figure 6

Figure 7

Figure 8

Figure 9

Figure 10

Figure 11
Role of median raphe serotonergic neurons in seizure induced death

Amelia Chen1, Molly Matkovich2,3, Rui Li3 & Gordon F. Buchanan3,4
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Introduction

- Sudden unexpected death in epilepsy (SUDEP) is defined as sudden, unexpected, non-traumatic, and non-drowning death in a patient with epilepsy.
- It is the leading cause of death among patients with refractory epilepsy and is second only to stroke in terms of potential years of life lost among all neurological conditions.
- SUDEP usually happens after a generalized tonic-clonic seizure.
- Interestingly, there is a sleep state-dependence of seizures: they rarely occur during the rapid eye movement (REM) sleep, thus suggesting that REM is protective.
- REM sleep and its characteristic theta activity are both regulated by serotonin (5-HT).
- Mice with a genetic deletion of serotonin have higher mortality rates.
- 5-HT is produced in several sites in the brain, including median raphe nucleus (MRN).

Objective

Determine whether stimulating MRN 5-HT neurons reduces seizure-induced death.

Method

Experimental Procedures

- Animal Surgery
- Three weeks of virus transfection
- Animal Trials
- 20 min habituation
- 10 min stimulation
- 3 days before MES.
- Mice were injected with AAV-ChR2 (activation of 5-HT neurons) or AAV-Arch (inhibition of 5-HT neurons).
- 2-3 days habituation before MES.
- Photo-stimulation lasts at least ten minutes before seizure induction, which is given during wake period.
- MES parameter: 30 mA, 0.2 s, 60 Hz, sine wave.

Results

Effects of optogenetic manipulation of MRN 5-HT neurons

Fig 1. Effects of activation of MRN 5-HT neurons at different frequencies via ChR2. (a, b) EEG power spectral density (a) and EEG power at different frequency bands (b) during and after 8 Hz stimulation in MRN-ChR2 mice. (c, d) A summary of EEG power spectral density (c) and EEG power at different frequency bands (d) during 1 Hz, 2 Hz, 4 Hz, and 8 Hz stimulation. All values shown have been subjected to baseline correction.

Fig 2. Effects of ChR2-mediated inhibition of MRN 5-HT neurons on EEG. (a, b) EEG power spectral density (a) and EEG power at different frequency bands (b) during and after stimulation. All values shown have been subjected to baseline correction.

Activation of 5-HT neurons decreases mortality rate in MES seizure mode

Fig 3. Verification of virus expression. (a, b) Expression of Arch-YFP (green) and TpOH (red) in median raphe from a Pet1-Cre MRN-Arch mouse. (c, d) Expression of ChR2-mCherry (red) and TpOH (green) in median raphe from a Pet1-Cre MRN-ChR2 mouse. Scale bars in (a, c), 200 μm; in (b, d), 50 μm.

Fig 4. Time-frequency analyses from one mouse that survived an MES seizure (a), and from one that died (b).

Fig 5. Effects of manipulation of MRN 5-HT neurons on MES outcome. (a) Seizure severity (extension-flexion (E/F) ratio) of MRN-ChR2 and MRN-Arch mice after at least 10 min stimulation. (b, c) Relationship between E/F ratio and EEG power changes at delta and theta bands relative to baseline for MRN-ChR2 mice (b) and MRN-Arch mice (c). (d) Mortality rate of MRN-Arch mice and MRN-ChR2 mice after MES. Numbers represent n’s.

Summary

- Activation of MRN 5-HT neurons via ChR2 affected the brain EEG in a stimulation frequency dependent manner.
- Inhibition of MRN 5-HT neurons increased delta power, but reduced theta power.
- Manipulation of MRN 5-HT neurons affected the outcome of MES seizure.

Conclusion

More mice survived MES seizure when MRN 5-HT neurons were activated compared to when 5-HT neurons were inhibited.

Future Directions

- Explore the role of 5-HT in other seizure models.

References


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Exploring genetic interactions between an epilepsy mutant and Alzheimer’s disease in flies

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1Dougherty Valley High School, 2Haddonfield Memorial High School, 3The University of Iowa

Introduction
Alzheimer’s Disease is a neurological disorder that affects 1 in 10 people over the age of 65. This condition has been linked to improper processing of the APP (amyloid precursor protein) and is known to be associated with widespread neurodegeneration and epilepsy. In Drosophila, another gene in the Planar Cell Polarity (PCP) complex called prickle (pk) (Figure 1a) has been associated with both of these phenotypes. When the prickle-spiny-legs isofrom (pk^{sple}) is mutated, the fly exhibits seizures which mimic those found in human PRICKLE patients (Ehaideb et al., 2016). Conversely, when the prickle-prickle isofrom (pk^{apl}) is mutated, preliminary data suggests that widespread neurodegeneration is observed in the Drosophila brain. Further connections between Alzheimer’s and PCP were found in previous work by Soldano et al. (2013), who demonstrated that the Van gogh (Vang) gene also interacts with appl (the Drosophila orthologue of APP) both genetically and physically during neurodevelopment (Figure 1b). All three genes, Vang, appl, and pk have been associated with neuronal connectivity; thus, we sought to determine whether the pk^{sple} isofrom interacts genetically with appl.

Methods and Materials
1. Genotypes assayed: WT (+/+), pk^{sple}pk^{sple} (sple/sple), appl^{apl}appl^{apl}, and appl^{apl}appl^{apl};sple/sple
   - All outcrossed to a w1118 background
2. Perform two 2-hour pre-lays to stimulate lays and synchronize embryo aging
3. Prepare 14-16 hour embryos for staining by removing chorions with bleach
4. Fix embryos in a 4% paraformaldehyde
5. Remove vitelline membranes by vigorously shaking embryos in methanol
6. Use immunohistochemistry (IHC) to stain for 22C10, a marker for peripheral neurons, and Fasciculin II (FasII), a marker for motor neurons
7. Image embryos with confocal microscopy and quantify the number of neuronal defects in each line

Preliminary Results

Figure 1. (1a) A schematic showing the PCP proteins Vang and Prickle potentially interacting with the Alzheimer’s protein Appl inside a neuron to promote proper neuronal development. (1b) This graph investigates the interaction between the appl^{apl} mutant and multiple mutants in the PCP complex during the development of the mushroom body of Drosophila. Soldano et al. demonstrated that the appl gene shows statistically greater disruption to proper neuron development when vang gene is also disrupted, hence, proving appl and vang genetically interact with each other. (figure adapted from Soldano et al., 2013)

Results (cont.)

Conclusions
- No defects were observed in any of the genetic lines: +/+, sple/sple, appl^{apl}appl^{apl}, and appl^{apl}appl^{apl};sple/sple
- Given that only 4.7% of embryos imaged by Tao, Manak, Sowers et al., had neuronal wiring defects, our study was likely underpowered and requires more samples to potentially reveal defects
- There is also a possibility of no genetic interaction between appl and the sple isofrom of prickle
- Alternatively, the phenotype of these mutants may be revealed when looking at later developmental stages in Drosophila

Future Directions
- Improve techniques to maximize the number of imageable embryos
- Determine whether there is an interaction between prickle and appl in mice

References

Figure 2. Staining of PNS and VNC using 22C10 antibodies. Asterisks indicate normal neuron extension portions (B) depicts a sple mutant with neuron extension defects (Tao, Manak, Sowers et al., 2011).

Figure 3. IHC of Drosophila embryos showing normal neuronal connectivity, all stained with the antibody 22C10. Brightness and contrast are modified for ease of viewing.

Figure 4. The graph shows the number of neuronal defects in each line.

Research Objective
To investigate the potential genetic interaction between an epilepsy mutant (pk^{sple}) and an Alzheimer’s gene (appl) during embryonic neuronal development
Background
Pancreatic neuroendocrine tumors (PNETs)
- Rare and slow growing cancers
  - Often not diagnosed until advanced
  - Limited treatment options for metastasis
- Better understanding of genes and pathways behind PNET pathogenesis needed for improved biomarkers and therapies

RABL6A
- Novel cancer-promoting protein upregulated in PNETs (Hagen et al., 2014)
- Mechanisms of action only partly understood
  - Kinome analyses (unpublished) suggest it activates CDK16 and EphA2 kinases

Objective: To test the hypotheses that...
1. RABL6A regulates CDK16 and EphA2
2. CDK16 and EphA2 can be inhibited by the drugs dabrafenib (Phadke et al., 2017) and ALW-41-27 (Amato et al., 2014), respectively, in PNET cells.

Methods
- Knocking down RABL6A in PNET cells
  - Transfect TSA cells with plasmids
  - Collect viruses from TSA cells
  - Infect Bon-1 cells with viruses
- Performing drug response assays
  - Plate control and infected Bon-1 cells for drug assay
  - Add drug, wait five days, and take readings
  - Freeze remaining cells into pellet for Western blot
  - Run gels and transfer gels onto nitrocellulose
  - Add antibodies and develop Western blot

Conclusions
- RABL6A promotes p27-S10 phosphorylation, possibly through CDK16 activation
- ALW-II-41-27 effectively suppresses PNET cell growth while dabrafenib selectively reduces BON-1 viability

Future Directions:
- Is CDK16 required for p27 regulation by RABL6A?
- Determine if CDK16 loss or overexpression alters the effect of RABL6A knockdown on p27 expression and S10 phosphorylation
- Investigate the role of other p27 kinases, such as AKT, in the RABL6A-p27 relationship
- Validate drug actions by performing kinase assays

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References
Validation of next-generation sequencing and applications in sex-specific genetic analysis in autism

Katherine Dong¹, Taylor Thomas², & Jacob J. Michaelson, Ph.D.²
¹Novi High School, Michigan; ²Department of Psychiatry, University of Iowa

Background

Autism Spectrum Disorder
• Autism spectrum disorder (ASD) is a neurodevelopmental disorder
• Repetitive behaviors and difficulties with social communication (Ferri, Abel, & Brodkin, 2018)
• Exact etiology unknown
• Complex condition → polygenic, influenced by rare and common variations (Gaugler et al., 2014)

Sex bias in ASD
• Sex bias with 4:1 male to female ratio (Wertling, 2016)
• Cause is unclear, multiple theories
  • Female protective effect (FPE): females are more protected from ASD than males
  • Sex hormones may have influence

Methods: Validation of Next-Generation Sequencing

Primer Design
• Primers designed using sequence around variant (indel in this case)
• Alternate sequence: indel being validated and compared to reference sequence

Sanger Sequencing
• Sanger sequencing used to sequence the fragment
• PCR using primers
• Amplify sequence with indel
• Gel electrophoresis confirmed correct fragment size

Results:
• Observed indel from the NGS sequence was not a variant in the sample, but an error in the NGS process

Sex-Specific Genetic Analysis in Autism

Methods:

CADD Scores → Combined Annotation-Dependent Depletion
• Deleteriousness of a variant (Rentzsch, Witten, Cooper, Shendure, & Kircher, 2018)
• Maximum CADD score per gene used for analysis
• Selected genes involved in sex hormone pathways and autism categories 1–6 from SFARI Gene database

Significance Tests
• Wilcoxon rank sum tests and t-tests on maximum CADD scores for each gene
• Identify significantly different scores between severe ASD male and female probands
• Significant genes on sex chromosomes filtered out

Results:

Table 1: Genes with significantly different max CADD scores between ASD males and females in Wilcoxon rank sum or t-test

<table>
<thead>
<tr>
<th>Gene</th>
<th>Genotype</th>
<th>Sex</th>
<th>SHBG Max CADD Score</th>
<th>Mean severe ASD males (n=106)</th>
<th>Mean severe ASD females (n=112)</th>
<th>p-value</th>
<th>Adj. p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALAD</td>
<td>wild type</td>
<td>female</td>
<td>0.9048</td>
<td>0.8569</td>
<td>0.6382</td>
<td>0.0052</td>
<td>0.0132</td>
</tr>
<tr>
<td>HSD11B2</td>
<td>wild type</td>
<td>male</td>
<td>0.7669</td>
<td>0.7579</td>
<td>0.6382</td>
<td>0.0031</td>
<td>0.0094</td>
</tr>
<tr>
<td>TRPM1</td>
<td>wild type</td>
<td>female</td>
<td>0.9657</td>
<td>0.9048</td>
<td>0.6382</td>
<td>0.0023</td>
<td>0.0055</td>
</tr>
<tr>
<td>ZFYVE28</td>
<td>wild type</td>
<td>male</td>
<td>0.7669</td>
<td>0.7579</td>
<td>0.6382</td>
<td>0.0031</td>
<td>0.0094</td>
</tr>
</tbody>
</table>

Note: Significant adj. p-value on Wilcoxon test

Conclusions

• Deleteriousness of some sex hormone genes differ between ASD males and females
• May contribute to FPE and sex bias
• Future studies investigating these genes
• Observed indel validated
• Important to validate variants → Validate variants found in computational analyses

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References
Video Games can be used to educate people about flood prevention and mitigation.

INTRO:

- Video games are a medium that enhance user engagement and encourage learning
- Globally, and in Iowa especially, flood alerts are very common: it is of the utmost importance for residents to make educated decisions based on real-time water body data, such as finding shelter, evacuating, and planning ahead
- The use of this game gives users an opportunity to teach themselves flood protection and mitigation techniques, such that they and their belongings are protected in the event of a flood.

METHODS:

- Design
  - Developed in plain, engine-less JavaScript
  - Created to seamlessly integrate real time flood data with game logic to create an educational yet enjoyable user experience
  - Use of simple, colorful graphics and easy to interpret menu system make the game appealing to anyone with any video gaming background
- Google Maps API Integration
  - The entire game is based on the Google Maps API's map overlay system
  - Tiles are overlaid on top of a real-time Google Map
  - This not only allows for IFIS data integration but allows for the second main feature of the game, its global scale
- Global adaptability
  - A main feature of the game is its changing user-by-user experience
  - Each new player can select to play their game anywhere in the world, using the game's automatic level generation along with the Google Maps API and global flood data.

RESULTS:

- Game engine structure beginning to be developed
- Accounts for future inclusion of planned features, such as global flood data and global scalability
- Concrete game design centered around optimally entertaining and educational experience for the user

FUTURE IMPLICATIONS:

- Once fully developed, this game will provide an educational experience for the user, allowing them to experiment with different flood remediation techniques
- The game will hopefully be able to eventually reach all its initial goals, including global scalability and global flood data incorporation

REFERENCES/ACKNOWLEDGEMENTS


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3D Printing of Tunable Piezoelectric Components via Ceramic Stereolithography
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1. Department of Mechanical and Industrial Engineering 2. Millard North High School

**Background**

- A big part of my project is additive manufacturing, commonly known as 3D printing
- Most people know about one 3D printing method, fusion deposition modeling or FDM
  - Plastic filament is melted into layers that stack together
- Stereolithography is another 3D printing method that uses an ultraviolet light and photosensitive materials like liquid resin
  - The UV light hardens certain areas of each resin layer, creating a solid shape (Chen et al, 2019)
- Stereolithography allows printing with materials like ceramics
  - Ceramics both can have piezoelectric properties and be biocompatible, but they can also be very brittle
- Piezoelectric properties mean that a change in pressure generates an electric charge, and vice versa
  - This allows ceramics to have medical applications, often as some kind of sensor (Chen-Glasser et al, 2018)
- Ceramics are hard to shape using traditional manufacturing
  - FDM doesn’t work, as the melting point of ceramics is too high to be practical
- This makes stereolithography the best option

**Method Application**

**UV Light Curing**

**Pure BTO Sample**

**Copper Tape**

**Connection to Oscilloscope**

**Prototype Pressure Application Setup**

**Results (pt. 1)**

- **Method Planning**
  - Using Autodesk Inventor, I 3D modeled a plan for the testing setup. The top screw puts a constant pressure on the sample, which is measured by an oscilloscope connected to the wires. Oscilloscopes measure the change in electrical signals. The bottom screws act as a clamp, so the setup can be used for any thickness sample.

- **Research Question**
  - What is the effect of adding a zinc oxide dopant to a barium titanate sample?
  - Is there a significant difference in their electromagnetic/dielectric properties?
  - Is there an effect on the piezoelectric properties?

- **Results (pt. 2)**
  - The dielectric properties stayed consistent all the way through our samples
  - Overall, the different samples gave very similar results
  - Adding a ZnO dopant should allow more customization of the sensor material
    - For example, by adding ZnO, we should be able to add density to the sample with minimal sensitivity loss
  - In this case, the density stayed the same, while the sensitivity did have a drop
    - Adding 2% of the dopant did not have a significant enough effect
  - Another possible reason for the minimal change could be the method of dispersal
    - In our trials, the ZnO was completely mixed into the BTO
    - In other trials, it is mixed in as a gradient through the piece
  - In future trials, we should try different dispersal methods to see if we can achieve a greater difference

- **References**

- **Acknowledgements**
  - I greatly appreciate the guidance and support of Dr. Song and his research group, including Li He. I thank the Belin-Blank Center, the National Science Foundation, and the SSTP program. Also, thank you to our Residential Assistants and our seminar leaders.
Introduction
Floods are a prevalent problem throughout the world, causing destruction of infrastructure and loss of life. In fact, flooding results in more deaths than other natural disasters including tornadoes, hurricanes, and lightning [4]. A main cause of death in relation to flooding is vehicle accidents that occur because roads can be covered with deep, fast-moving water [5]. Another cause of death is being inside homes and other buildings when a flood occurs [2].

Leading Flood-Related Hazards for People: Water Depth & Water Velocity

Objective

Our project aims to reduce the number of deaths from flooding by providing individuals with alerts when a flood is occurring. The project will focus on helping people inside vehicles and buildings.

Depth Sensing (via Ultrasonic Sensor):

To find the water depth, we used an Arduino and an ultrasonic sensor (HC-SR04). The circuitry is shown below.

The ultrasonic sensor returns two distances in centimeters: the water depth and the height difference between the sensor and the water. These two measurements taken are shown below.

Velocity Sensing (via LSPIV):

To find the water surface velocity, we used a smartphone application based on Large-Scale Particle Image Velocimetry (LSPIV). LSPIV tracks particles on the surface of the water and finds their velocity. Using the height above the water, the app is able to scale the velocity from LSPIV into meters per second [3].

Percentage of Flash Flood Victims Based on Activity [2]
Vehicle (VE) – 646, Outside/Close to Streams (OU) – 220, Campsite/Recreational Area (CA) – 72, Permanent Building & Mobile Home (BH) – 40

1036 Total Victims

Velocity Sensing (via LSPIV)

The picture on the right shows the setup that was used to collect the data. The red dot is where the smartphone (iPhone) was.

The ultrasonic device was tested for accuracy. The device performed with an error of ± 1.6%.

The LSPIV app was tested with a variety of camera heights and water velocities. The uncertainty for the tested conditions ranged from ± 6.5% to ± 8.7%.

Future Research

- Integration of the ultrasonic sensor with the smartphone
- Improvement of the LSPIV application:
  - Reliable scaling of velocity vectors based on height
  - Faster speed of imaging
  - Moving interrogation windows
- Communication between the application and the ultrasonic sensor

Acknowledgements:
I would like to thank Dr. Marian Muste for his guidance on this project. Additionally, I would like to thank IIHR, Byota Tsubaki, and the team at the Model Annex.

References:

For more resources, scan the QR code below.
Improving the selectivity of polydicyclopentadiene membranes by adding different activators

Benjamin Hong1, Katherine Sulaitis2, B.S., Ned Bowden2, Ph.D.
1 East Brunswick High School, 2 Department of Chemistry, University of Iowa

Introduction

EPA-EE (Eicosapentaenoic acid ethyl ester) and DHA-EE (docosahexaenoic acid ethyl ester), two derivatives of fish oil, require expensive separation methods, such as distillation or chromatography. Membranes offer an alternative solution that is significantly more cost effective. The purpose of this project is to create a membrane composed of polydicyclopentadiene (PDCPD) capable of separating fatty acids with high flux ratios between desirable and non-desirable molecules.

Methods

Dicyclopentadiene (DCPD) has a highly reactive alkene group, that allows it to engage in ring-opening metathesis polymerization.

<table>
<thead>
<tr>
<th>Grubbs catalyst</th>
<th>Activator</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dissolve in dichloromethane</td>
<td>2 Hours @ 50°C</td>
</tr>
</tbody>
</table>

The membrane acts similarly to a coffee filter, where larger particles are unable to pass through but smaller particles can.

The selectivity of the membranes was tested by adding p-nitrobenzaldehyde and triphenylmethane and finding their flux ratios. Since triphenylmethane is a larger molecule, less of it should permeate through.

Overall, the Grubbs first generation catalyst performed much better than the second generation catalyst. The second generation catalyst membranes were significantly thinner and possessed many traits that were not ideal for separations.

Results

We found that using tetrachlorocyclopropene gave us the best p-nitrobenzaldehyde to triphenylmethane flux ratio of about 5.4:1 when used in a 1:1 ratio with the Grubbs first generation catalyst. This is an improvement from the other membranes, which typically had flux ratios of only about 3:1.

Implications

The membranes studied in this study are unique in their ability to separate molecules by cross-sectional area rather than molecular weight. This provides an alternative way of separating fatty acids, which has depended on the same methods for decades. In order to ensure that the membranes work optimally for EPA-EE and DHA-EE, it is important that in the future the membranes are tested for their selectivity with these molecules. Also, the permeation rate could be improved by applying pressure or changing temperature, which could provide a new industrial method of separating fatty acids that is less expensive and equally, if not more, effective than current methods of separation. Hopefully, this will create a successful method of separating fatty acids that is both efficient and inexpensive.

References

- Gupta A, Bowden NB. Separation of cis-fatty acids from saturated and trans-fatty acids by nanoporous polydicyclopentadiene membranes. ACS Applied Materials & Interfaces. 9:2328-2333. PMCID: 35957736. DOI: 10.1021/am509264y

Acknowledgments

I would like to thank Professor Ned Bowden and Katherine Sulaitis, the graduate student I worked with, for spending the time to guide me for this research project. I wish them and the rest of the Bowden research group the best of luck in their future endeavors. I would also like to thank the Belin-Blank center for providing me with the resources and opportunity for this project.
Objective: Find Genetic Cause of Orofacial Clefts

Results

Wild Type | Mutant
---|---
Lysine | Glutamic acid

Novel variation found at position 55749667 on chromosome 12. Although SIFT predicted it to be tolerated and PolyPhen anticipates benign, its CADD score was 23.7, which ranks it among the top 1% of deleterious variants.

Wild Type | Variant
---|---
Glycine | Arginine

Rare, known variation (rs780604190) [MAF=3.985e-6] found at position 55748780 on chromosome 12. This variant was also classified as tolerated and benign for SIFT and PolyPhen, but its CADD score was 22.4, which means it is predicted to be among the top 1% of deleterious variants.

Methods

- **Collect Samples**
- **DNA Extraction**
- **Primer Design**
- **Sanger Sequencing**
- **Gel Electrophoresis**
- **Polymerase Chain Reaction**
- **Sequence/Segregation Analyses**
- **Functional Studies**
- **Confirm with Animal Subjects**

**HOPE Summary**

- Charge of AA swaps from positive to negative
- Heavily disturbs protein interaction and formation
- This particular AA is likely in contact with other proteins
- Vastly changes protein interaction
- Glutamic acid is slightly smaller than Lysine

**Location** | **Codon Change** | **Amino Acid Change** | **PolyPhen** | **SIFT** | **Provean** | **CADD**
---|---|---|---|---|---|---
chr12: 55749667 | K(AAG)>E(GAG) | Lys 337 Glu | Benign | Tolerated | Neutral | 23.7 (top 1%) 
chr12: 55748780 | G(GGA)>R(AGA) | Gly 214 Arg | Benign | Tolerated | Neutral | 22.4 (top 1%)

Conclusion

This study found two variants that could affect the protein’s function, and both are predicted to be among the top 1% of deleterious mutations. Both variants demonstrated a change in charge, which would impact protein interaction. There is a good chance that these mutations contributed to the formation of OFCs in the patients.

Future Work

- Troubleshoot and redesign primer for exon 1 of this gene
- Test predictions on Zebrafish embryo to determine whether this variation actually has a severe effect
- Determine if the variants are functional using migration assays in keratinocytes and mesenchymal cells

Acknowledgements: I would like to thank the Butali Lab for allowing me to conduct research. I appreciate Dr. Azeez Butali for his support and for allowing me to work in his lab. Tamara Busch and my lab group were also crucial to help me learn how to properly conduct research. I would also like to thank the Belin-Blank Center for hosting the SRT program. Finally, for the samples used in this study, I thank the families in Ghana, Ethiopia, and Nigeria. This work was supported by NICHD R01-R08 Grant DE023778 and Robert Wood Johnson Foundation Grant number 72429 (AB).

Citations:

Testing the role of the mitochondrial calcium uniporter in pain, learning and anxiety behavior in mice

Yuting Huang, Leonid Shutov, Jake Rysted, Maria Pattschull, Yuriy Usachev

Introduction/Background:
Synaptic plasticity is the ability for synaptic connections to become stronger or weaker based on one’s experience. Long-term exposure to a certain stimulus makes neurons easily excitable to generate a response. Synaptic plasticity is involved in almost all neuronal activities such as anxiety behaviors, memory formation, pain processing and neurological diseases like epilepsy.

The mitochondrial calcium uniporter (MCU) is a calcium channel on the inner membrane of mitochondria. Calcium controls the release of neurotransmitters. By elongating the time of high cytoplasmic calcium level, MCU enhances synaptic connections. Therefore, MCU can be a potential therapeutic target to treat neurological diseases by modulating synaptic plasticity. The effects of MCU on synaptic plasticity of neurons that process different types of information need to be determined before the application of medicine that targets MCU.

Methods:
By comparing the differences between MCU knockout and wild type mice in different behavioral tests, the effects of MCU on different brain functions can be discovered.

1. Elevated plus maze was used to test the effect of MCU on anxiety behaviors. Mice were given two choices: open arms where they should feel safe from light, height and potential predators; closed arms where they should feel protected in the dark and enclosed environment. The more a mouse explores the open arms, the less stressful it is.

2. In the novel object recognition test, mice were habituated to the arena, familiarized with two objects and allowed to explore one of the familiar objects and a novel object. The more a mouse explores the novel object, the stronger its recognitive memory is. In cued fear conditioning test, mice were first trained to associate foot shocks (a fearful stimulus) with a tone in a certain context. Their fearful experience by the context or the sound cue.

3. CFA was injected into the hind paws of mice to induce inflammation. The pain responses (paw withdrawal, licking or shaking) to mechanical and thermal stimuli were measured through von Frey and Hargreaves tests respectively. The more sensitive they are, the more severe pain response they develop.

Results:

- Elevated plus maze results:
  - Figure 1: A. Cumulative durations mice spent in the open arms. B. Frequencies of entries mice made to the open arms. These two graphs show that MCU-KO mice had similar anxiety-related behavior to WT mice.

- Novel object recognition test results:
  - Figure 2: A. Differences in cumulative duration mice spent around the familiar and novel objects. The graphs show that MCU-KO mice were not significantly better in recognitive memory than WT mice.

- CFA-induced inflammatory pain test results:
  - Figure 3: A. The average time for different genotypes to respond to a visible light beam (active intensity=20) after injections. B. The average nociceptive thresholds to a mechanical stimulus. MCU-KO resembled WT in developing inflammatory pain.

Conclusions:
MCU deletion did not cause a statistically significant effect on the anxiety-related behavior, memory or inflammatory pain reception of mice (p-values>0.05). However, MCU-KO tended to do better in recognizing novel objects, but become more hypersensitive to thermal stimuli in the presence of inflammation. These findings were underpowered and need further validation. Hypersensitivity to heat should be addresses when applying medicine that targets MCU.

References:

- Hargreaves--thermal and von Frey--mechanical

Anxiety
Elevated plus maze
Memory
Cued fear conditioning
Novel object recognition test
Pain reception
MCU & synaptic plasticity
CFA-induced inflammatory pain test
Hargreaves--thermal
von Frey--mechanical

Figure 1: A. Cumulative durations mice spent in the open arms. B. Frequencies of entries mice made to the open arms. These two graphs show that MCU-KO mice had similar anxiety-related behavior to WT mice.

Figure 2: A. Differences in cumulative duration mice spent around the familiar and novel objects. The graphs show that MCU-KO mice were not significantly better in recognitive memory than WT mice.

Figure 3: A. The average time for different genotypes to respond to a visible light beam (active intensity=20) after injections. B. The average nociceptive thresholds to a mechanical stimulus. MCU-KO resembled WT in developing inflammatory pain.
INTRODUCTION

Autism Spectrum Disorder (ASD) • neurodevelopmental disorder • challenges with social skills, behavior, and communication • affects 1 in 59 children in the US (Fombonne, 2018)

There is a need for a more accessible test to analyze gene expression in ASD. Gene expression data is usually lacking in sample size, limiting the power of the study (Abrahams & Geschwind, 2008). Metabolic screening cards could make gene expression analysis more accessible. Data can be collected from more individuals and provide a better sample of genetic issues in ASD.

Metabolic Screening Cards • typically used during newborn screening to detect metabolic disorders • simple finger prick • benefits • more convenient way to collect a sample (no need for a phlebotomist) • provides a broad range of data (Karlsson, Guthenberg, von Döbeln, Kristensson, 2003).

METHODS

Quantitative reverse transcription PCR (RT-qPCR) is used when the starting material is RNA. In this method, RNA is first transcribed into complementary DNA (cDNA) by reverse transcriptase from total RNA or messenger RNA (mRNA). The cDNA is then used as the template for the qPCR reaction to detect, characterise and quantify nucleic acids for numerous applications.

RESULTS

Table 1: RNA Qubit Results

<table>
<thead>
<tr>
<th>Sample Type</th>
<th>Concentration (ng/µl)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Human Brain Tissue</td>
<td>24</td>
</tr>
<tr>
<td>Human Blood From Metabolic Screening Cards (#1)</td>
<td>3.27</td>
</tr>
<tr>
<td>Human Blood From Metabolic Screening Cards (#2)</td>
<td>7.89</td>
</tr>
</tbody>
</table>

Figure 3: Extraction & RT-qPCR Process

Figure 4: RNA Bioanalyzer Results (Human Brain Tissue)

RNA INTEGRITY NUMBER (RIN): 8.40

Figure 5: RNA Bioanalyzer Results (Human Blood From Metabolic Screening Card #1)

RNA INTEGRITY NUMBER (RIN): 3.00

Figure 6: RNA Bioanalyzer Results (Human Blood From Metabolic Screening Cards #2)

RNA INTEGRITY NUMBER (RIN): 2.10

CONCLUSION

• Total RNA was successfully extracted from the metabolic cards, however it is low quality.
• cDNA can be successfully reverse transcribed from RNA from metabolic cards
• The presence of B2M was detected from the reverse-transcribed cDNA by traditional PCR

FUTURE DIRECTIONS

• Develop an RT-qPCR protocol to qualitatively detect the amount of the gene of interest (as opposed to the traditional PCR, which just detects presence/absence)
• Use this method for genes implicated in autism to analyze gene expression

REFERENCES


ACKNOWLEDGEMENTS

Thank you to Dr. Jacob Michaelson, Taylor Thomas, the Michaelson Lab, the Belin-Blank Center, and SSTP for their help and this opportunity!
Characterizing a mutation of the mitochondrial membrane protein

**AKAP1 in intellectual disability**

He Jiang¹, Yujia Liu², Ronald A. Merrill², Stefan Strack²

¹Princeton Intl. School of Math and Science, Princeton, NJ
²Department of Pharmacology, University of Iowa Carver College of Medicine, Iowa City, IA

Abstract

Mitochondrial dynamics is driven by a protein named Drp1. An anchoring protein on mitochondrial outer membrane called AKAP1 regulates this process by interacting with Drp1’s two enzymes, PKA and CaN. Their interactions are shown to influence neural development in mice. In this study, we try to characterize how AKAP1 mutations might affect human neural development. We focused on how one AKAP1 mutation identified in a 3-year-old patient contributes to intellectual disability. Specifically, we approach this goal by refining a two-step purification process to obtain the desired AKAP1 proteins. We construct plasmids to produce AKAP1 with GST-tag and his-tag fused before proceeded to immunofluorescent staining for mitochondria (cyan), AKAP1 (green), and promoting cell cycle progression. ATP production. However, it is also “powerhouses” of cells because of it

**Backgrounds**

Fig 1. “The Powerhouses”—

Mitochondria in mammalian cell. Mitochondria are known as the “powerhouses” of cells because of its ATP production. However, it is also responsible for other functions such as maintaining calcium homeostasis and promoting cell cycle progression. (Image credit: Pearson Education, 2009)

Fig 2. Electron microscopy image of mitochondria. Mitochondria dynamics refer to the constant equilibrium of fission and fusion. Dynamin-related protein of (Drp1) drives this process. (Image credit: www.sciencedirect.com)

Fig 3. AKAP1::PKA::CaN regulates the function of Drp1. AKAP1 (A-Kinase Anchoring Protein 1) is an anchoring protein located on the mitochondrial outer membrane. It binds to two enzymes, CaN that activates and PKA that inactivates Drp1, which is a protein that causes mitochondrial fission.

Objective

A 3 years-old female patient in Spain was found to carry compound heterozygous AKAP1 mutations. Patient clinical features:

- Intellectual disability
- Autism

Experimental Approaches:

AKAP1 subcellular localization (V33G) / Mitochondrial morphology / AKAP1 protein turnover / AKAP1::CaN interaction

Results

Fig 7. A typical Coomassie stain image of nickel column purification results (R124H). Before the purification, our proteins should exist in the supernatant after lysis because of its solubility. We can see during the purification, most uninvolved proteins are washed off. In the 100mM final elution, we can perceive the existence of our desired protein (AKAP1); though some still remains on the nickel bead (last two lanes). This suggest a higher concentration of imidazole can be use to elute in the future.

Fig 8. Protein elutions compared with BSA standards. The signal intensity of the standards and elutions from Coomassie stains (left) are compared using ImageJ. Then the protein concentrations are calculated (right). Elutions are diluted to same concentration before proceeding with the next purification.

Fig 9. Fast-green staining of GST-glutathione purification and brain lysate pull down results

We can see the existence of AKAP1 on beads, proving a successful purification despite the uneveness in their amount. From the pull-down, most protein in brain lysate end up in the flowthrough, while the binding is weak.

Fig 10. Western blotting of brain lysate pull down results, probing for GST and 2CaN.

We can see the existence of various protein in the flowthrough, but not much in the actual pull down. We detect 2CaN in the flowthrough, but not in brain lysate or pull down. Since bands appear, the antibodies should be functional, while degradation or low protein concentration might account for no bands.

Fig 8. Protein elutions compared with BSA standards. The signal intensity of the standards and elutions from Coomassie stains (left) are compared using ImageJ. Then the protein concentrations are calculated (right). Elutions are diluted to same concentration before proceeding with the next purification.

Methods

Rosetta cell transformation

Protein Production: Cell cultures & IPTG induction

Protein Extraction: Cell lysate

Conclusion & Future Direction

- For this specific project, we have finalized the two-step purification process to obtain desired AKAP1 protein. To boost the signal strength, we can use higher protein concentration might account for no bands.

Acknowledgement

Secondary Student Training Program
Stefan Strack Laboratory
Dr. Alberto Fernandez Jaen M.D.

References

The design and implementation of a low-cost solution for cluster computing with MATLAB on Docker Swarm

Kaibo Tang¹,², & Chris W. Schwarz²
¹The Stony Brook School, Stony Brook, NY, ²National Advanced Driving Simulator, University of Iowa, Iowa City, IA
kaibo-tang@uiowa.edu

Introduction

The objective of this study is to design a low-cost solution for cluster computing with MATLAB.

Hypothesis 1: Performance of the cluster will be positively correlated with:
- Number of paralleled tasks on a single machine;
- Total number of machines involved in the cluster.

Hypothesis 2: Cluster > Parallel

Conclusion

This study manifests the feasibility and promising performance of simultaneously running multiple containerized MATLAB scripts in an on-premise computer cluster. The advantages of Docker compared to other solutions are listed in Table 2.

Table 2. The advantages of Docker compared to other solutions.

<table>
<thead>
<tr>
<th></th>
<th>Docker</th>
<th>HPC Pack</th>
<th>Parallel Server</th>
<th>pMATLAB</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cost</td>
<td>$0</td>
<td>$9,722/40</td>
<td></td>
<td>$0</td>
</tr>
<tr>
<td>OS Requirement</td>
<td>/</td>
<td>Windows Server (2)</td>
<td>/</td>
<td>/</td>
</tr>
<tr>
<td>Coding</td>
<td>N/A</td>
<td>N/A</td>
<td>No</td>
<td>N/A</td>
</tr>
<tr>
<td>Performance</td>
<td>Highly</td>
<td>N/A</td>
<td>Yeast</td>
<td>N/A</td>
</tr>
</tbody>
</table>

[1] The cost is comparable to running on a single computer.
[3] Windows Server is only required for head nodes and worker nodes. OS requirement for workstation nodes is Windows 10 Pro, Education or Enterprise.

The study also paved the way for deploying ndaqTools onto all the idle machines at NADS which, embedded with a data access interface to the filer, will significantly increase the data reduction efficiency.

Acknowledgment

I would like to express my special thanks to Dr. Schwarz and Dr. Brown for having me at NADS and for the opportunity to put my crazy idea of creating an HPC cluster into practice. Secondly, I would like to thank my parents who never fail to take my phone calls when I am in need. Last, I would like to thank my friend Rong Lu for her suggestion on the art design of this poster.

References

Swatski, S. (2014). Investigating the Use of pMatlab to Solve the Poisson Equation on the Cluster maya(Tech.). Baltimore, MD: The University of Maryland, Baltimore County. doi:10.13016/M2CC0TX59

Result

This study manifests the feasibility and promising performance of simultaneously running multiple containerized MATLAB scripts in an on-premise computer cluster. The advantages of Docker compared to other solutions are listed in Table 2.

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Swatski, S. (2014). Investigating the Use of pMatlab to Solve the Poisson Equation on the Cluster maya(Tech.). Baltimore, MD: The University of Maryland, Baltimore County. doi:10.13016/M2CC0TX59
Effect of diet on gut microbiome and metabolic pathways

Siddhartha Kalala¹, Yuanchao Ye²,³, Mohamad Mokadem²,³

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2. Department of Internal Medicine, Gastroenterology and Hepatology, University of Iowa, Iowa City, IA
3. Fraternal Order of Eagles Diabetes Research Center, University of Iowa, Iowa City, IA

Research Question: What is the effect of diet on gut microbiota composition and bacterial metabolic pathways?

Background

▪ Gut microbiota has been lately associated with shaping many human health conditions, including obesity and its associated metabolic disorders.
▪ It has been previously reported that obese humans and animals have different microbial composition residing in their gut. Furthermore, transferring microbiota from an obese individual to a leaner one was shown to induce obesity in the recipient irrespective of the type of diet.
▪ Finally, diet has been found to be one of the main factors molding our gut microbiota.

Methods

C57 Blk/6j on Normal Diet C57 Blk/6j on High Fat Diet
23 Weeks Later
Ceca of mice were snap-frozen in liquid nitrogen and stored at -80°C.
DNA was extracted from cecum and sequenced at the V3–V5 region of the 16s rRNA and was processed by DADA2 in R to form OTUs at 97% similarity level.
Taxonomic profile data was then analyzed using METAGENassist.

Discussion/Conclusion

1. High fat diet induces minimal but significant changes in the gut microbiota at the family level. An increase in Desulfovibrionaceae, Peptostreptococcaceae, Streptococcaceae, and Verrucomicrobiaceae, as well as a decrease in Erysipelotrichaceae and Lachnospiraceae has been associated with a state of obesity and metabolic derangement.
2. More pronounced changes were observed at the genus level. A decrease in Bacteroides and Alistipes, and an increase in Lactococcus and Parabacteroides was detected in high fat diet-fed mice. These bacterial genera have also been associated with a state of obesity and metabolic derangement. Paradoxically, we observed an increase in Akkermansia, which has been attributed to a leaner, healthier state.
3. At the bacterial metabolic pathway level, we observed an increase in chitin and xylan degradation, dehalogenation, sulfate reduction and sulfide oxidation in high fat diet-fed mice compared to those on a regular diet. Many of these molecular reactions have been associated with increased utilization of alternative energy source. These findings suggest that a high fat diet induces a newer gut environment that is more avid for energy harvest.

Acknowledgements

I would like to thank the Belin-Blank Center, SSTP, Dr. Mokadem and his research group, and the University of Iowa for providing me with the opportunity to do this research.

References

Patients' Consent For Supervised Pelvic Exams Under Anesthesia, Performed by Medical Students

Krisha Keeran, Emily Jacobs MD, Karen Summers MPH, Rachel Mejia DO
Department of Obstetrics and Gynecology, University of Iowa Hospitals and Clinics

Research Objectives
- Determine the proportion of patients who give consent for a medical student to perform a supervised pelvic exam under anesthesia
- Analyze the possible variables that may impact a patient's choice to consent for a supervised pelvic exam by a medical student under anesthesia

Background
- Medical students often perform pelvic exams for educational purposes at training hospitals.
- Eight states have prohibited nonconsensual pelvic exams.
- When surveyed, 62% of patients indicated that they would give consent to medical students to perform pelvic exams under anesthesia.
- It does not appear that this update to the consent form inhibits learning opportunities for medical students.
- Institutions in other states can use this information when planning to update their consent forms and address concerns.

Methods
- Fields examined: patient age, surgical procedure, surgical OB/GYN division, patient acquiring consent.
- Personal acquiring consent by the patient consented to a supervised pelvic exam under anesthesia.
- Consent rates found to vary by division (p = 0.001).
- Evidence of relation between consent rate and division (p = 0.001).
- Percentages found to vary by division (p = 0.001).

Conclusions
- 75% of patients consented to a supervised pelvic exam under anesthesia performed by a medical student.
- No evidence of relation between consent role and consent rate (p = 0.497).
- Evidence of relation between procedure approach and consent rate (p = 0.001).
- Evidence of relation between division and consent rate (p = 0.001).

Acknowledgements
Special thanks to Karen Summers, Dr. Mejia, Dr. Jacobs, all members of the Department of Obstetrics and Gynecology, the Belin-Blank Center, the Secondary Student Training Program for their assistance in making this research study possible.

References
Quantification of the Mechanical Properties of Crystalline 9-Anthracene Carboxylic Acid Ribbons

Vedanta Kompella¹, Thiranjeewa Lansakara², Alexei Tivanski²
Kennedy High School, Cedar Rapids, IA¹; Department of Chemistry, The University of Iowa²

Background
9-Anthracene Carboxylic Acid (9-ACA) is a crystalline material which changes its shape upon exposure to light ([4+4] Photodimerization)

- Forms Ribbons at the Micorscale
- Reverts to its original form (eventually)
- Ribbons twist (2-4 min), then untwist (5-15 min)
- Can be repeated for multiple cycles
- Ideal for application as actuators in small machines because unaffected by illumination conditions

Atomic Force Microscopy (AFM)
- AFM uses a sharp tip to indent samples
- Data is force vs tip’s indentation depth
- Use models which fit the data to determine mechanical properties
- Use Johnson-Kendall-Roberts (JKR) Model to find the Young’s Modulus (measure of elasticity)

Objectives
1. How does elasticity of Ribbons change after exposure to light?
2. What’s the difference in elasticity between Macro Crystals and Ribbons?

Methodology
We often experienced low yields of ribbons, and even then, they tended to agglomerate (making them unusable for the AFM).

Drying the ribbons faster (via a desiccator w/vacuum or smaller drops on slides) seemed to stop the latter.

Achieving more accurate concentrations and adding more solution (like 3.8 mg in 2 ml) even slower seemed to increase yield.

Macro Crystals Synthesis: Slow Evaporation
- 5.7 mg 9-ACA dissolved in 1.0 mL filtered ethyl acetate
- vial sealed with a polyethylene lid pierced by a needle
- crystallized as ethyl acetate evaporated over many days
- Crystals ground up before use in the AFM (very rough)

UV Irradiation
- Used Metal Halide Lamp (200 W, 10%) for irradiation
- UV Light filter: 360 nm
- Exposed for 1-2 min

9-ACA exhibited fluorescence (both forms)

Micro Ribbons Synthesis: Floating Drop Method
- 1.9 mg 9-ACA dissolved in 1.0 mL filtered ethyl acetate
- slowly added to surface of MilliQ purified H₂O in Petri dish
- covered and left in the dark for 48 h (for solvent evaporation)
- Pipetted onto a quartz slide for AFM use

Conclusions
Implications
- Higher elasticity of photo reacted ribbons explains why ribbons don’t shatter, but twist
- Fluorescence seemed to fade away over multiple cycles (like previous studies)
- Photobleached Ribbons didn’t revert to the monomer form, showed no fluorescence (unlike more robust nanorods of 9-ACA)
- Similar elasticity of Ribbons and Crystals – probably probing on same crystallographic plane (002 or 004, unknown)

Future Directions
- Understanding why ribbons have large Young’s Modulus and relation to crystal planes
- Finding hardness of ribbons and macro crystals for engineering applications
- Seeing how elasticity and hardness changes over multiple cycles and with photobleaching
- Calculating optical to mechanical energy conversion factor (see usefulness as actuator)
- Finding mechanical properties of better derivatives (such as 4-Flouro 9-ACA)
- Finding the mechanical properties of other Micro ribbons for comparison (9-Methyl Anthracene, 4 chlorocinnamic acid, etc.)

Acknowledgments

References
INTRODUCTION

- Attention Deficit Hyperactivity Disorder (ADHD) is one of the most commonly diagnosed neurodevelopmental disorders.
- Behaviorally, ADHD is characterized by inattention, hyperactivity, or a combination of the two.
- Due to decreased frontal lobe efficiency, individuals with ADHD also exhibit deficits in various cognitive processes like inhibitory control (Tannen et al., 2004).
- To assess inhibitory deficits, task-switching procedures are often used.
- Previous work using a task-switching paradigm has demonstrated increased response time and error rate performance in ADHD youth (Cepeda et al., 2000).
- To ameliorate the cognitive deficits in ADHD, many individuals are prescribed stimulant medication (e.g., Ritalin, Adderall).
- Questions persist regarding whether medication helps to alleviate some of these deficits.

OBJECTIVES

1) Examine whether ADHD children exhibit impaired task-switching performance compared to non-ADHD children and how medication helps to alleviate some of these deficits.
2) Assess how the correspondence between medication status on Day 1 and Day 2 affects overall performance.

PROCEDURE

Day 1
ON
OFF
Control

Day 2
ON
OFF
Control

Figure 2. Randomization procedure for all groups: participants with ADHD completed the tasks either on or off medication on Day 1, and the opposite on Day 2.

RESULTS: RESPONSE TIME (RT)

On Day 1, the reaction times for switch trials are longer than repeat trials. The switch costs (switch RT - repeat RT) are similar for all groups.

On Day 2, the reaction times for switch trials are longer than repeat trials. The switch costs (switch RT - repeat RT) are similar for all groups but are smaller compared to Day 1.

RESULTS: ERROR RATE (ER)

On Day 1, the error rate of the OFF group was substantially higher compared to the ON and control groups. The error rates for switch trials were higher than repeat trials across all groups. The switch costs remain similar across all groups.

On Day 2, the error rate of the ON-ON group was smaller compared to all other ADHD groups. Switch trials still remain less accurate than repeat trials across all groups. The switch costs also remain similar across all groups.

REFERENCES


ACKNOWLEDGMENTS

Special thanks to Jonathan Schacherer and Dr. Eliot Hazeltine for their guidance on this project and the Belin-Blank Center for their support. This project was partially funded by the U of Iowa GPSG program.
Effect of mesocarnivores on nesting bird abundance

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Background

- Urban environments play a key role in conserving biodiversity (1-3).
- Studies of relationships between different groups of urban species such as mesocarnivores and nesting birds are needed to build knowledge of urban biotic communities and support the design of urban biodiversity conservation approaches.

Research Objective: To identify effects of mesocarnivore presence on bird nesting guild abundance

- Expected effect to vary with mesocarnivore species and nesting guild
- Presence of ground-dwelling mesocarnivores will negatively influence ground and shrub nester abundance and have no significant link with tree nester abundances.
- Tree-climbing mesocarnivores will negatively impact tree nesters.

Methodology

- Mammal sites were identified by arraying three transects along an urbanization gradient across the study area (4).
- Divided transects into 10 km² blocks within which we selected 4 sample sites using random sampling stratified by land cover.
- Sampled mesocarnivores on each of the resulting 38 sites by deploying motion-sensitive trail cameras for 30 days in July (2017-2018) and identified 9 species. Considered mesocarnivore species present if detected by camera on a site.

- Identified 3-5, 50-m bird survey sites within 1 km of each mammal site using land-cover based stratified random sampling.
- Surveyed sites at least twice in June and July, 2017-18, recording counts of all species seen or heard. We recorded 59 native species.
- Used counts to indicate breeding-season abundance of each species on each site.
- Aggregated counts to bird nesting guild (tree, shrub, ground, primary cavity, secondary cavity) to identify abundance of birds in each guild on each birding site.
- Matched these with mesocarnivore detections to identify presence of mesocarnivores at bird sites.
- Analyzed resulting dataset using Wilcoxon rank-sum tests to identify significance of differences in nesting guild abundance with and without each mesocarnivore.

Results

- Abundance of most nesting guilds did not differ significantly when most mesocarnivore species were present.
- Tree nester abundance was lower when red foxes were present, but not significantly ($p = 0.10$).
- Secondary cavity nester abundance was significantly lower when house cat (*Felis catus*) and Virginia opossum (*Didelphis virginiana*) were present ($p < 0.05$).

Key Findings

- Most nesting guilds are uninfluenced by mesocarnivores
- Cat and opossum may reduce secondary cavity nester abundance
- Red fox may reduce tree nester abundance.

Conservation Implications

- Conservation of secondary cavity and tree nesters should consider cat, opossum, and red fox management.
- Overpopulation of these guilds or their rarity in resource-rich habitats may signal the need to manage these mesocarnivores for population control or to reduce predation.

Future Studies

- We used nesting songbird abundance and mesocarnivore occurrence estimates that were not adjusted for detectability. Future analyses should use detectability-adjusted estimates.
- Inspect similar relationships across all seasons instead of just breeding season
- Consider other environmental attributes that could influence songbird abundance and mesocarnivore presence

References


Acknowledgements

I’d like to thank Heather Sander, Brandon Macdougall, Adam Skibbe, and Steve Hendrix for all the mentorship, help, and support they graciously provided me during these five weeks of research.
Optimizing gene delivery for osteodifferentiation by varying ratio of pFGF-2 to pBMP-2

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Introduction
- Certain types of bone fractures cannot heal spontaneously and therefore require therapeutic intervention (Einhorn and Gerstenfeld, 2014).
- FGF-2 and BMP-2 are proteins that regulate the differentiation of osteoblasts (bone-forming cells) from uncommitted stem cells.
- Co-delivery of genes encoding for BMP-2 and FGF-2 synergistically enhances bone formation. (Atluri, Seabold, Hong, Elangovan, & Salem, 2015)

Research Objective
- Maximize cell viability and transfection efficiency of PEI-pDNA complexes
- Determine ratio of pFGF-2 and pBMP-2 that optimizes bone formation

Nanoplex Fabrication
- Fabrication of PEI-pDNA complexes. The positively charged amine groups (N) in PEI form electrostatic interactions with negatively charged polynucleotides (P) leading to DNA allowing for formation of complexes.

Nanoplex Characterization
- Characterization of pBMP-2, pFGF-2 and pEGFP using gel electrophoresis. Plasmid DNA was restricted digested with ageI and run on 1% agarose gel. Lengths of pDNA fragments matched standard values.

Effect of co-delivery on protein production
- Previous studies have found significant increases in BMP-2 production with co-delivery of pBMP-2 and pFGF-2 (Atlin et al, 2015)
- However, no significant differences in either BMP-2 or FGF-2 production were found.

Evaluation of Cell Viability
- Relative viability of varying densities of cells transfected with 1ug PEI-pDNA. Formazan production from MTS assay measured spectrophotometrically. Density of 10,000 cells had highest viability 24 hours post-transfection.

Evaluation of Transfection Efficiency
- Mean fluorescent intensity of varying BMSC densities. BMSCs successfully transfected with pEGFP measured using flow cytometry at 48 hours post-transfection. Non-transfected cells were included as a reference. No significant differences were found in mean fluorescent intensity.

References
Einhorn, TA, Gerstenfeld LC. Fracture healing: mechanisms and interventions. Nat Rev Rheumatol. 2015 Sep;11(9):554-560. doi: 10.1038/nrrheum.2014.166

Acknowledgements
Many thanks to Tim Acri, Dr. Salem and the Belin-Blank Center for making this project possible.

Conclusion
- Cell viability was highest when 1 ug of nanoplexes was added. Transfection efficiency decreased with increase in cell density.
- However, cell viability 24 hours post-transfection increased at higher cell densities.
- Thus, parameters of 1 ug of nanoplexes and 11,000 cells/well seeding density were used for ELISA assays.
- ELISA results did not indicate significant differences in protein production through varying ratio of pFGF-2 and pBMP-2 complexes.
- Expanding the range of concentrations and repeating the procedure may lead to conclusive findings.

Future Directions
- Further study of osteogenic potential of free nanoplexes versus that of nanoplexes seeded on scaffolds
- Nanoplexes are source of osteoinductive factors.
- Scaffolds provide mechanical support necessary for osteoconduction.
- Thus seeded scaffolds may be studied to better investigate potential clinical applications.
- Findings on optimal parameters (quantity of PEI-pDNA complexes and cell density) may be applied for future in vitro studies
Methodology

Two B-2(200) WLS fibers ("Fiber 1" and "Fiber 2") were cut and polished. Both were irradiated for sixteen hours at the cesium-137 source at the University of Iowa’s RadCore facility. Fiber 1 was allowed to recover naturally with exposure to ambient light, while Fiber 2 was exposed to UV light in sub-ten minute intervals. Spectra of both were taken using a xenon PX-2 laser processed by SpectraSuite software, the spectrum data from which was plotted using MATLAB, integrated, normalized, and checked for percent difference and systematic/random error.

Findings

- Ultraviolet treatment is definitively superior to natural recovery, leading to recovery of radiation damage at a rate (especially given Fiber 2 started out more severely damaged than Fiber 1) significantly higher than the natural -- as can be seen in Fig. 5.
- This outpaces the rate at which damage is incurred to the fibers, implying that novel new methods for repairing radiation damage using UV treatment during intrinsic calorimeter inactivity between particle collisions could be utilized to negate existing light attenuation.
- Upon receiving a dose of 21.5 kilogray of radiation, the fiber's light transmittance had dropped to 26.3% of pre-irradiation. 80% was attained at 32.5 hours, and over approximately 43 hours from start, the fiber returned to its peak (100%) transmittance.
- This implies that it is possible to completely remove the need to replace optical fibers -- which would necessitate significant time and budgetary concerns -- or continuously recalibrate detection devices by preventing damage from becoming a problem in the first place.
- This first fiber is a 59.7cm long Kuraray B-2(200) wavelength-shifting (WLS) fiber, and was left untreated with UV light to obtain the natural recovery rate from radiation damage.
- Upon receiving a dose of 21.5 kilogray of radiation, the fiber's light transmittance had dropped to 26.3% of pre-irradiation. 80% was attained at 32.5 hours, and over approximately 43 hours from start, the fiber returned to its peak (100%) transmittance.
- Upon receiving a dose of 21.9 kilogray of radiation, the fiber's light transmittance had dropped to 20% of pre-irradiation. Over 9.6 hours, the fiber returned to 80% of baseline transmittance.

Fiber 1

- Ultraviolet treatment is definitively superior to natural recovery, leading to recovery of radiation damage at a rate (especially given Fiber 2 started out more severely damaged than Fiber 1) significantly higher than the natural -- as can be seen in Fig. 5.
- This outpaces the rate at which damage is incurred to the fibers, implying that novel new methods for repairing radiation damage using UV treatment during intrinsic calorimeter inactivity between particle collisions could be utilized to negate existing light attenuation.

Fiber 2

- The second fiber is a 60cm long Kuraray B-2(200) WLS fiber and was treated with UV light in sub-10min direct exposures, having spectra taken every ten minutes with continuous measurement.
- Upon receiving a dose of 21.9 kilogray of radiation, the fiber's light transmittance had dropped to 20% of pre-irradiation. Over 9.6 hours, the fiber returned to 80% of baseline transmittance.

Fig. 1: Percent difference between transmittance of recovered fiber and never-irradiated fiber. Green shading represents the region of systematic and statistical error.

Fig. 2: Transmittance of light through the damaged fiber as a percentage of the peak value versus time (measured in days).

Fig. 3: Transmittance of light through the UV-treated fiber as a percentage of the peak value versus time (measured in hours).

Fig. 4: Incident light intensity versus wavelength for the first fiber, recovering over the week of 5/28 to 6/7.

Fig. 5: Percent difference between transmittance of recovered fiber and never-irradiated fiber. Green shading represents the region of systematic and statistical error.

Fig. 6: Transmittance of light through the damaged fiber as a percentage of the peak value versus time (measured in hours).

Fig. 7: Transmittance of light through the UV-treated fiber as a percentage of the peak value versus time (measured in hours).

Acknowledgements

I'd like to thank my mentor, Dr. James Wetzel, and the rest of the HEP group at the University of Iowa for guiding me in my research -- as well as SSTP and my parents for allowing me to reach this opportunity in the first place.
A Serious Game for Flood Mitigation: Automated Level Generation

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Background
• Flood simulations have long been a concern to both conduct studies and raise awareness for such studies on open sourced sites. Though it had been conducted before, this study seeks to create a simulator in a online video game format that would semirealistically demonstrate a terrain on the bank of a river during the time of a flood.
• It is shown that such studies is able to raise awareness among individuals not previously acquainted with the topic, as show by a study conducted on students. (Felicio et al., 2014).
• A previous system called Stop Disasters was an inspiration for the design of the game, though with several modifications (Blasko-Drabik et al., 2013).
• The program is created mainly with JavaScript with HTML. The JavaScript reads from the Google Maps API and is central to most of the programming involved in the designing of this game.
• The project is divided into two sections, one section for autogenerating a level of the player's choice and another for laying out the graphics of the level per information from the first section. This study seeks to complete the former.

Method
• The generation of levels requires the program to read the pixels of the map and generate a corresponding map. The process of generating a map is beyond the scope of this presentation.
• The program generates on click a region on the map that can be manipulated by the player to conform with the player's desired playing field. The player selects the desired region allows the program to analyse the region. This is done by converting the Google Maps into a static image suing the Google Maps Static API. The program removes labels and minor roads to allow for ease of analysis.
• The program divides each pixel into a rgba (Red-Green-Blue-alpha) value and identifies it as a type of terrain since the map already colors it. These can then be processed by the game and generated into a level. The division into terrain types is precise since for most of Google Maps similar types of constructions (i.e. buildings, roads, etc.) are marked with similar colours, though there are exceptions.
• The terrain types can then be mapped to a tiling system and tiled into a game level. That is the main involvement of the second section and is beyond the scope of the first.

Examples
(Bottom Center) The program analyses the pixels of the image and maps them to an array defining the terrain types. It then returns the rgba values of a pixel and the terrain type it maps to. Since in Google Maps with labels removed separate terrains are indicated with colour, it becomes possible to identify them this way. The result is show in the demonstration designated by the arrow.

(Center & Right) The selection of a Google static image on the map and the analysis of the pixels as demonstrated in the code above are shown. The selecting section is draggable and editable by mouse movements and is therefore flexible. The selection also results in the program analysing the pixels of the static image and identifying the type of block represented by the pixels, as show.

Further Developments
• The two sections of the game remain to be integrated in order to form a complete simulation.
• Many aspects of the game remain incomplete and require modification in order to make it sufficiently realistic. Several other serious games have already become sophisticated enough such that they are realistic on a 3D scale (Khoury, et al., 2018).
• Details regarding the workings of a disaster remain to be implemented.
• The program has inaccuracies with mapping since there are exceptions to colouring on Google Maps with some of the pixels marked with unusual rgba values between an ordinary value that can be identified and a generic tile.

Sources
• Khoury, M., Gibson, M., Savic, D., et al., 2018, A Serious Game Designed to Explore and Understand the Complexities of Flood Mitigation Options in Urban–Rural Catchments, Water.
Development of probe to detect and identify damage by reactive neurotransmitter metabolites

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BACKGROUND

3,4-dihydroxyphenylacetaldehyde (DOPAL) in Parkinson’s Disease (PD)

In the brain, the neurotransmitter dopamine (DA) undergoes enzyme-mediated oxidation to produce a toxic metabolite called 3,4-dihydroxyphenylacetaldehyde (DOPAL).

The “catecholaldehyde hypothesis,” suggests that DOPAL has shown to play a role in the pathogenesis of Parkinson’s Disease (PD) by damaging dopaminergic neurons through several toxic mechanisms:

- auto-oxidizes to form quinones that stimulate production of reactive oxygen species.
- lipid peroxidation of cell, vesicular, and mitochondrial membranes.
- stimulates alpha-synuclein protein to bind to tropomyosin receptor kinase B, which interferes with neurotrophic activities.
- binds covalently with proteins through a Michael addition mechanism.

It is hypothesized that DOPAL will bind to bovine serum albumin in the control experiment as well as certain proteins in the N27 cell lysate via Michael addition mechanism.

OBJECTIVE

Main objectives:

- to detect and/or identify the protein targets of DOPAL.
- generate a method to investigate the proteins damaged by a reactive metabolite of dopamine that is thought to contribute to PD.

FUTURE DIRECTIONS

- Repeat initial experiments to confirm validity of results.
- Visualize N27 lysate after addition of citric acid on SDS-PAGE.
- Identify DOPAL protein targets using a proteomics-based approach with the Agilent 1290 series HPLC interfaced with an Agilent 6530 QTOF mass spectrometer.
- Develop research for PD therapeutics related to protein targets of DOPAL.

CONCLUSION

The concentration of N27 lysate protein with DOPAL was higher than that with sodium phosphate buffer, which indicates protein modification activity by DOPAL. However, the SDS-PAGE analysis shows that there were no notable differences among the three samples before the addition of citric acid. Moreover, samples with citric acid were not visible. Further experimentation is needed to validate the hypothesized Michael addition by DOPAL.

REFERENCES


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Examining an iterative development of reward functions to generate autonomous driving models using reinforcement learning

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Introduction

- **Machine learning** is the training of a model on data sets before it is used on a test data set to generate a predicted result.
- **Reinforcement learning** uses a reward function to encourage certain behaviors.
  - If a model adheres to the coded guidelines, then new models can be built off of it to explore other behaviors (Qiang & Zhongli, 2011, p. 1143).
  - Pre-training a model can decrease training time by reducing the initial learning curve (Kim, Cha, Ryu, & Jo, 2019, p. 2).
- Using past data and trends is practical for the processing of large amounts of signals (Moon, Cheong, Yeom, & Woo, 2019, p. 345).

- **Amazon Web Services’ DeepRacer**
  - Virtual car undergoes training for user-inputted time and then evaluation.

- **Research Objectives**
  - Determining an optimal combination of parameters and their respective rewards in the model.
  - Building off of previous models to determine how past iterations can influence future performance.
  - Observe applicability of model on track segments.

Methods

1. **Track curvature**
   - Relative Distance
     \[ d = \frac{|x'y'' - x''y'|}{|x'|^2 + |y'|^2} \]
   - Bezier Curves
     \[ K = \frac{x^3y - x^2y'}{2} \]
   - Vector Calculations
     \[ \cos \theta = \frac{<u,v>}{|u||v|} \]

2. **Progress per step**
3. **Speed**

Results

- Figure 1. The stages of reinforcement learning.
- Figure 2. Deep Racer car.
- Figure 3. Track visualization.
- Figure 4. Curvature representations.
- Figure 5. Model development cycle.
- Figure 6. Distribution of times for evaluation laps in various model series.
- Figure 7. Track paths taken by a virtual car during training period for various initial reward functions.
- Figure 8. Representation of path taken for an evaluation lap for various initial reward functions.
- Figure 9. Cumulative rewards for initial reward functions during training period.

Development Cycle

- New reward function
- Clone and modify reward function
- Revise base model
- Training period
- Evaluation
- Log Analysis

Conclusion

- **Vector calculations** for curvature yielded the fastest and most accurate performance.
- Rewarding progress relative to steps was effective.
- Models developed as **newly initialized reward functions** performed better than corresponding cloned models.
- Successive iterations of reward functions did not always produce improved models.

Future Directions

- Build off of successful models to optimize car path and speed in both virtual and physical Deep Racer.
- Explore the use of iterative learning models in navigation based solely on sensor input.
- Apply reinforcement learning reward functions to situations where certain behaviors are favored.

Acknowledgements

Thank you to my mentor Dr. Denise Szecsei, the Belin-Blank Honors Center, and SSTP for this opportunity. An additional thanks to the University of Iowa’s Computer Science Department, the Information Technology Services, and the AWS DeepRacer team for their assistance throughout this project.

References

Endometrial cancer (EC) is the most common gynecologic malignancy, causing over 11,000 deaths every year.

Progesterone is a key tumor suppressor in endometrial cancer. After binding with progesterone receptor (PR), progesterone can inhibit cell growth, promote apoptosis, and facilitate cell differentiation.

Existing progestin-based therapy has a low response rate in poorly-differentiated endometrial cancer due to the loss of PR expression.

HDAC inhibitors (HDACi) are the most common PR upregulation pathway. Specific HDACi can be designed to solely target the HDAC2 gene instead of the HDAC1 gene. These results verify that the downregulation of HDAC2 can upregulate the expression of PR and its downstream gene.

In vivo study

Validation in other cell lines, and study the effect on cell proliferation
Chromatin immunoprecipitation (ChIP) assay to verify the direct PR repression by SETDB1 and HDAC2
Transcriptome analysis to study broader effect of SETDB1 and HDAC2 downregulation

References

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Figure 6.2 (right) Confirmation of the DNA knockout

Figure 5. Enzyme digestion of the empty vector. Confirming the size of vector plasmid pHR5S Puro.

Figure 7. Assessing HDAC2 knockout at the protein level by Western Blot. HDAC2 increases PR and its downstream gene PGRA/B.

Figure 2. SETDB1 and HDAC2 are unfavourable prognostic markers for endometrial cancer. The statistical results suggest that the highest SETDB1 and HDAC2 expression correlates with the worst survival of EC patients (adapted from the Human Protein Atlas).

Figure 1. A suggested model of PR expression regulated by SETDB1 and HDAC2 in endometrial cancer. PR is the progesterone response element which is recognized by the progesterone-activated progesterone receptor. In endometrial cancer cells, PR is downregulated, and HDAC can upregulate PR expression. Our hypothesis is that the HDAC2 and SETDB1 genes are novel PR repressors.

Methods

**Objective**

The objective of this study is to investigate the mechanism of PR downregulation. Specifically, we want to confirm that the SETDB1 gene and HDAC2 gene are two novel progesterone receptor repressors.

**Background**

- Endometrial cancer (EC) is the most common gynecologic malignancy, causing over 11,000 deaths every year.
- Progesterone is a key tumor suppressor in endometrial cancer. After binding with progesterone receptor (PR), progesterone can inhibit cell growth, promote apoptosis, and facilitate cell differentiation.
- Existing progestin-based therapy has a low response rate in poorly-differentiated endometrial cancer due to the loss of PR expression.
- HDAC inhibitors (HDACi) are the most common PR upregulation pathway. Specific HDACi can be designed to solely target the HDAC2 gene instead of the HDAC1 gene. These results verify that the downregulation of HDAC2 can upregulate the expression of PR and its downstream gene.

**Methods**

**STEP 1** Vector preparation

**STEP 2** Ligation and transformation

**STEP 3** PCR selection of correct insertion

**STEP 4** Confirmation by sequencing

**STEP 5** 5% Gene Knockdown by RNA Interference

**Method 1**

**Method 2**

SETDB1 and HDAC2 genes are two novel progesterone receptor genes. Specifically, we want to confirm that the SETDB1 and HDAC2 genes are two novel progesterone receptor repressors.

**Results**

**Conclusion**

- Downregulation of HDAC2 and SETDB1 restores functional PR expression
- HDAC2 and SETDB1 are novel PR repressors
- HDAC2 and SETDB1 are potential targets in endometrial cancer

**Applications**

If the SETDB1 gene is verified to be the bona fide PR suppressor, the drug can be designed to inhibit SETDB1 expression, and therefore, restore normal PR function.

If the HDAC2 gene is proved to be the bona fide PR suppressor, there can be improvement in HDAC inhibitors. Specifically, HDACi can be designed to solely target the HDAC2 gene instead of the whole HDAC family including (from HDAC1 to HDAC11). In that case, several side effects caused by the misfunction of other HDAC genes due to HDACi can be prevented.

**Future Directions**

- Validation in other cell lines, and study the effect on cell proliferation
- Chromatin immunoprecipitation (ChIP) assay to verify the direct PR repression by SETDB1 and HDAC2
- Transcriptional analysis to study broader effect of SETDB1 and HDAC2 downregulation
- In vivo study

**Figures**

- Figure 1: A suggested model of PR expression regulated by SETDB1 and HDAC2 in endometrial cancer.
- Figure 2: SETDB1 and HDAC2 are unfavourable prognostic markers for endometrial cancer. The statistical results suggest that the highest SETDB1 and HDAC2 expression correlates with the worst survival of EC patients (adapted from the Human Protein Atlas).
- Figure 3: Forming small hairpin RNA (shRNA) in target cells after transfection to degrade target gene. Viral, with shRNA target DNA is transcribed into cells, and the shRNA is processed into short interfering RNA (siRNA). One strand of the shRNA duplex is loaded into the endogenous RNA-induced silencing complex (RISC). This guide strand siRNA then localizes RISC to the mRNA of the target genes (SETDB1 and HDAC2). The cleaved mRNA is degraded by other endogenous nucleases.
- Figure 4: CRISPR-Cas 9 mechanism. Single-guide RNA (sgRNA) with a short “guide” sequence attaches to target sequences of DNA in a genome. The RNA also binds to the Cas9 enzyme which cuts the DNA at the targeted location.
Diversity of a Recently Discovered Gene with Under-Explored Implications on Nitrogen Cycling

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Introduction

- The nitrogen cycle is extremely important in wastewater treatment plants (WWTP).
- Recent literature presents potential presence of nitric oxide dismutase (nod) that may exhibit oxygenic activity believed to be impossible in aerobic WWTP conditions1, 4, 5
- 2NO → N₂ + O₂ dismutation by methane oxidation coupled with nitrate reduction2
- Significant implications for global climate change2
- Diversity and abundance of nod gene in Iowa wastewater & soil reported in this study

Methods

Figure 1: Quantitative PCR analysis of nod gene copies and 16S gene copies. Values determined with averaged data of two extractions from environmental samples. Error bars set at minimum and maximum. Much lower than expected abundance with ±0.085% nod genes in samples.

Results

- qPCR data shows evidence of nod gene presence in all environmental samples. Unexpectedly low nod abundance is observed in samples, significantly lower than ~1–2% nod gene abundance found in prior literature5.
- Found two distinct clusters of Iowa nod genes indicate some diversity of nod genes in Iowa wastewater & soil. Clusters include both wastewater and soil samples, supporting similar nod variations to be in both types of samples.
- nod variations in different geographic locations tending to cluster most strongly amongst each other suggests nod variations tend to differ in distinct global locations.
- Some nod variations clustering more closely to distant geographic locations suggests that there are, in fact, nod variations that are present in different locations.

Conclusion

- Determining nod abundance and diversity in nitrogen–rich Iowa presents a step toward understanding the impact of nod in the nitrogen cycle on the local and global scale. Understanding nod will allow scientists and engineers to better develop wastewater treatment processes and potentially contribute to lowering greenhouse gas emissions which dominate the pressing global climate change issue.

Implications

Acknowledgements

I am grateful to Mattes Lab for guiding me in conducting my project. I would like to thank Professor Timothy Mattes for giving me the opportunity to work in his lab, Patrick Richards and Weilun Zhao for their guidance and commitment, and Jessica Ewalt for her assistance. Thank you to the Belin–Blank Center. This work was supported by NSF Grant 1802583.

References


Significant association between Dual-Path Platform® CVL assay and Soluble Leishmania Antigen ELISA in the diagnosis of canine leishmaniosis

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DPP® CVL assay is an efficient test that can accurately diagnose canine leishmaniosis, a potentially fatal disease, in the place of gold standard diagnostic tests, such as SLA ELISA.

Methods

1. Prepare antigen (2ug/mL) and coat wells. Block to prevent non-specific binding.
2. Add sample sera (1:500 dilution).
3. Add secondary antibody: rabbit anti-dog antibody. TMB substrate turns contents blue.
4. Stop reaction with H2SO4 acid. Read plate with Omega software.

Figure 2: A) Basic steps of ELISA and B) Unused DPP® assay (left) and positive reading on a DPP® assay (right)

Figure 1: A) Leishmania infantum parasites B) Female phlebotomine sand fly accessed on 7/10/19 from CDC/Frank Hadley Collins

Figure 3: Contents of a plate well throughout indirect SLA ELISA Accessed on 7/12/19 from Bio-Rad

Figure 4: Significant correlation between DPP® and SLA ELISA diagnostic results. Fisher’s Exact Test determined there was a significant relationship between DPP® diagnosis and ELISA diagnosis (***, p = 0.0001). It was found that DPP® had a sensitivity of 80% and specificity of 100%.

Figure 5: Significant correlation between ELISA optical density (O.D.) values and time to positive for DPP® test in our positive dogs. Ordinary Linear regression found a significant relationship between ELISA O.D. values and DPP® time to positive (r² = 0.4569, p = 1.695 × 10⁻⁶).

Figure 6: Significant ELISA O.D. difference between symptomatic, vaccinated dogs and asymptomatic, not vaccinated dogs. Ordinary One-Way ANOVA with Tukey’s multiple comparisons test showed only one significant difference (p = 0.0469) in mean values between symptomatic, vaccinated dogs and asymptomatic, not vaccinated dogs.

Results cont.

Results

DPP Diagnosis vs. ELISA Diagnosis

Comparing DPP Time to Positive to ELISA O.D. Value

ELISA O.D. by Clinical and Vaccine Status

Acknowledgements

I would like to thank the Petersen Lab, Belin-Blank Center, and the University of Iowa for providing such an amazing opportunity to aspiring researchers.

References


I would like to thank the Petersen Lab, Belin-Blank Center, and the University of Iowa for providing such an amazing opportunity to aspiring researchers.

Conclusions and Future Directions

• DPP® CVL assay is a reliable and valid diagnostic test that can be used on the field
• There is a significant increase in average O.D. as DPP® time to positive decreases
• Vaccinated, symptomatic dogs have more robust immune response, that is likely due to vaccine effects, when compared to asymptomatic, not vaccinated dogs
• Future studies can include:
  • Comparing ELISA O.D. values to DPP® Micro Reader values
  • Testing outside of the hunting dog population

Study Question

• What is the relationship between the leishmaniasis diagnostic results of the DPP® CVL assay and SLA ELISA?

Hypothesis

• There is a significant association between DPP® CVL assay and SLA ELISA results.

Background

• Approximately 100,000 new cases of visceral leishmaniasis (VL) each year, “fatality rate in developing countries can be as high as 100% within 2 years” (CDC)
• Caused by Leishmania donovani or Leishmania infantum (Larson et al., 2018, p. 381)
• Vectors: phlebotomine sand flies (Ready, 2014, p.148)
• Primary reservoir host: dogs- canine leishmaniosis (CVL)
• Endemic to hunting hounds in the US, passes along through vertical transmission only right now (Boggiatto et al., 2011, p.1)
• Current gold standard diagnostic tests are all lab tests; need field tests
• There is a significant association between DPP® and SLA ELISA

Hypothesis

• What is the relationship between the leishmaniasis diagnostic results of the DPP® CVL assay and SLA ELISA?

Hypothesis

• There is a significant association between DPP® CVL assay and SLA ELISA results.

Methods

1. Prepare antigen (2ug/mL) and coat wells. Block to prevent non-specific binding.
2. Add sample sera (1:500 dilution).
3. Add secondary antibody: rabbit anti-dog antibody. TMB substrate turns contents blue.
4. Stop reaction with H2SO4 acid. Read plate with Omega software.

Figure 2: A) Basic steps of ELISA and B) Unused DPP® assay (left) and positive reading on a DPP® assay (right)

Results

DPP Diagnosis vs. ELISA Diagnosis

Comparing DPP Time to Positive to ELISA O.D. Value

ELISA O.D. by Clinical and Vaccine Status

Acknowledgements

I would like to thank the Petersen Lab, Belin-Blank Center, and the University of Iowa for providing such an amazing opportunity to aspiring researchers.

References


I would like to thank the Petersen Lab, Belin-Blank Center, and the University of Iowa for providing such an amazing opportunity to aspiring researchers.
Learning From Profanity – Offensive Speech Detection via Transfer Learning

Xintong Yu¹,²; Infroj Shrestha, PhD²; Jonathan Ruser, PhD²; Padmini Srinivasan, PhD²
¹Phillips Exeter Academy, ²University of Iowa

Introduction
- Increasing propagation of offensive speech on social media.
- Significant investment from governments, companies, and researchers to regulate this phenomenon.
- While censorship curtails freedom of speech, unregulated offensive speech provokes hate crime and eventually jeopardizes a platform’s utility.

Offensive Speech
Personal attacks or degrades to another user. Offensive speech contains terms with recent or historical meaning relating to a particular gender, race, sexual orientation, or other characteristic of a user or group of users.

Related Work
- Popular classifiers include deep learning models such as CNNs, RNNs, as well as ensemble models.
- In the 2019 OffensEval (Zampieri, et al., 2019) task, the pretrained BERT model (Devlin, Chang, Lee, & Toutanova, 2018) achieves promising performance.
- However, the performance of the above models relies on enormous amount of task-specific training data, which poses a challenge since it is costly and time-consuming to create such datasets. We tackle this problem by transfer learning.
- Transfer Learning applies classification knowledge learned from a previous domain to a new domain (Pan et al., 2010).

Our Contribution
- We present a new transfer learning model that extracts features from another external text corpora to monitor offensive tweets.
- We demonstrate that the new approach is able to consistently improve the F-1 score of baseline models by approximately 5.39%.

Objectives
- Implement a variety of deep learning models as baselines, including the latest Google BERT model.
- Investigate the efficacy of transfer learning architectures and compare their performance with baseline models.

Data Description
The Offensive Language Identification Dataset (OLID) contains 13400 tweets for training and 860 tweets for test. Tweets are labeled as either Offensive (OFF) or Not-Offensive (NOT). (1) OFF - @USER Just block the dist. He’s not even worth this post. (2) NOT - @USER You are so sweet and adorable

Data and Methodology

Discussion
- The sentiment analysis dataset, due to the relative shortness of its tweets, does not produce reasonable accuracies and is thus not included in the results.
- For the toxicity dataset, all transferred models consistently outperform their respective baseline by an average of 5.39%.
- Transferred CNN model performs best with all layers trainable while other models involving Recurrent layers achieve higher F – 1 with only dense layers trainable. Intuitively, this is because CNN focuses on filtering keywords specific to each corpus, and RNNs overspill if all weights are fine-tuned.
- Notably, the transferred CNN model outperforms the BERT model by 0.69.

Conclusions & Future Work
We design transfer learning architecture to detect offensive speech in Twitter. The proposed method is able to consistently improve the performance of deep learning models. While CNN performs better with layers all trainable, models with RNN prefer only trainable dense layers. In the future we aim to experiment with other datasets for pretraining and implement more diversified transfer learning architectures.

Acknowledgement
Special thanks to Asad Mahmood, Osama Khalid, and all members of the computer lab for providing the guidance needed to complete this project. Special thanks to Dr. Lori Ithig and Dr. Duhita Mahatnaya for leading the Secondary Student Training Program.

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References


Glove: Global vector for word representation. Proceeding of the 2014 conference on empirical methods in natural language processing (EMNLP), (pp. 1532-1543).

Effects of potassium channel mutations on motoneuron morphology in *Drosophila* giant-neuron cultures

**Veda Amalkar¹, Jeffrey Zhang², Tristan O’Harrow³, Cassandra Burke³, Atulya Iyengar³, Chun-Fang Wu³**

¹Valley High School, ²Centerville High School, ³Department of Biology, University of Iowa

**INTRODUCTION**

- *Drosophila* are used as a model organism for their relatively small genome, short life cycle and ability to reproduce large numbers of offspring.
- Potassium channels play a vital role in neuronal function by restoring the resting potential after an action potential occurs.
- Cytochalasin B (CCB), a cell-permeable mycotoxin, blocks cytokinesis in cells without having an effect on nuclear division. In this experiment, CCB was used to create giant neurons in order to make neuronal growth more evident (Wu 1990).
- In vitro cultures are ideal for studying neuronal properties and analyzing altered mechanisms in mutants (Wu 1983).
- This experiment used *ether-a-go-go* (eg) and Shaker (Sh) mutants as well as a wild-type control.

**RESEARCH OBJECTIVES**

The primary objective of this experiment was to determine the changes in motoneuron morphology as an effect of potassium channel mutations in *Drosophila* giant-neuron cultures. Additionally, we observed the role of heat on neuronal growth in the cultures.

**METHODS**

1. **Virgin and egg collection**
   Virgin females were collected in the mornings while unconscious under CO2 and subsequently kept at room temperature for mating to occur.

2. **Culture preparation**
   Embryos were dechorionated and cells were extracted from 4-5 embryos per culture. The cells were then placed into culture medium which consisted of amino acids, glucose, CCB and other components to foster neuron growth.

3. **Microscopy and imaging**
   Pictures were taken over a span of fifteen days under both fluorescence and brightfield. Fluorescent images revealed the motoneurons and brightfield images allowed the neurites to be captured more clearly.

4. **Analysis of neuronal growth**
   After pictures of the cultures were taken, neurons were counted and categorized based on polarity. Additionally, terminal complexity of neurons was assessed. Finally, neuronal growth from cultures of different temperatures was compared.

**RESULTS**

- **Wild-type**
- **eg**<sup>¹⁰⁶</sup> (N=10)
- **eg**<sup>²</sup> (N=10)
- **Sh**<sup>¹⁰⁶</sup> (N=11)
- **Sh**<sup>²</sup> (N=12)

  - Cultures of all five genotypes were kept in both room temperature and high temperature (29°C) environments.
  - All genotypes had C164-GCaMP (Gα4-UAS system), a genetically encoded fluorescent calcium indicator, to drive fluorescence in motor neurons.

- **Polarity**
- **Terminal complexity**

- **CONCLUSIONS**
  - Motor neurons with mutations do not display higher terminal complexity.
  - **Terminal complexity**
    - Higher temperatures increase terminal complexity of neurons regardless of genotype.
    - Similar growth of the three terminal branch types was observed in all genotypes at room temperature.
      - Predominantly Type 1, followed by Type 2 and Type 3 respectively.
  - **Polarity**
    - Temperature change had a more drastic effect on Shaker neurons than wild type and eg.
    - Proportions of monopolar, bipolar and multipolar neurons in eg and Shaker neurons were similar.
    - There was a significant genotype effect on polarity between the mutant and wild-type cultures.

- **IMPLICATIONS and FUTURE DIRECTIONS**
  - Epilepsy, a common neurological disorder, occurs when potassium channels fail to regulate the neurons and cause repeated firing of signals.
  - Future work:
    - Breeding flies with different channel mutations together and culturing the neurons.

**REFERENCES**


**ACKNOWLEDGEMENTS**

I would like to express my gratitude to the members of the Wu lab and my peers at SSTP for supporting me throughout these 5 weeks. Thank you to the Belin-Blank Center and the University of Iowa for this amazing opportunity.
# The impact of demographic factors on baseline simulated driving performance

Alex Wang¹, Thomas Burt², Dawn Marshall², Timothy Brown²

¹Saratoga High School, ²National Advanced Driving Simulator, University of Iowa

## Objectives

The study compared the simulator driving performance of drivers of varying demographics. Specifically, we hypothesized:

- Speed will be higher for males than females.
- Speed will decrease with increasing age.
- Standard deviation of lane position (SDLP) will not be affected by driver sex.
- SDLP will have a parabolic relationship with driver age.

The study used 10,725 points of female data and 11,197 points of male data with the drivers aged between 16 and 67.

## Introduction

### Influence of Age

- Younger drivers generally underestimate risk factors and overestimate their ability (Borowsky et al., 2010); therefore, they are the age group most at risk for fatal crashes.
- Elderly drivers display greater inconsistency in maintaining headway and lateral position (Bunce et al., 2012) and drive slower when distracted (Horberry et al., 2006).

### Influence of Sex

- Younger men were more likely to engage in fatal crashes, but women had a higher risk of nonfatal crashes (Massie et al., 1995).

## Methods

### Baseline Simulated Driving

We used drive data from NADS-1 and miniSim under normal driving conditions, meaning that there were no external distractions and the driver was not drowsy or under the influence of drugs or alcohol.

### Data Analysis Process

<table>
<thead>
<tr>
<th>Raw data broken into 120-second chunks and reduced in MATLAB</th>
<th>Reduced data collected in a central repository</th>
<th>Microsoft Access to query data for relevant studies and variables</th>
<th>Data imported to MATLAB or plots and statistical tests</th>
</tr>
</thead>
</table>

Figure 1: Older drivers tend to drive slower and deviate less from the speed limit. Linear model for age and speed limit vs. speed: \( R^2 = 0.76 \) and coefficient of speed = -0.097

Figure 2: SDLP varies more for younger drivers and appears to decrease across age, but no model was found that accounts for variability of data. t-test: \( p = 0.12 \) and mean difference = 0.016

Figure 3: Speed is higher and varies more for males. t-test: \( p < 0.001 \) and mean difference = 1.26

Figure 4: SDLP between sexes is similar: t-test: \( p = 0.12 \) and mean difference = 0.016

## Results

### Influence of Age

- Older drivers tend to drive slower and deviate less from the speed limit. \( R^2 = 0.76 \) and coefficient of speed = -0.097
- SDLP varies more for younger drivers and appears to decrease across age, but no model was found that accounts for variability of data. t-test: \( p = 0.12 \) and mean difference = 0.016
- Speed is higher and varies more for males. t-test: \( p < 0.001 \) and mean difference = 1.26

### Influence of Sex

- Both sexes should be included when looking at speed, but unnecessary when looking at SDLP.
- Both sexes should be included when looking at SDLP, but unnecessary when looking at speed.

## Conclusions/Implications

The results of this study serve to direct future simulated driving studies in their sampling of drivers. It is imperative to consider teen drivers because they tend to drive differently from the rest of the population.

### In terms of sex:

- Both sexes should be included when looking at speed, but unnecessary when looking at SDLP.

### In terms of age:

- Drivers of all ages should be included when looking at both speed and SDLP.

## Future Directions

- Consider other factors on driving performance such as experience and miles driven per year.
- Analyze effects on other variables such as standard deviation of speed and lane crossings.

## Acknowledgements

A special thanks to Dr. Brown, Ms. Marshall, Thomas Burt, Kevin Tang, and all the other staff at the National Advanced Driving Simulator. Thank you to the Belin Blank Center and the University of Iowa for allowing me to attend this amazing opportunity at SSTP.

## References


An analysis of corn stover production with image recognition across an agriculture field

Eddie Wang1; December Weir2; Caglar Koylu, PhD1,2; Dr. Mark Linderman, PhD1,2
Palo Alto High School1 - Department of Geographical and Sustainability Sciences, The University of Iowa2

Introduction & Background

- Remote sensing is when a sensor, usually a camera, is attached to a drone or satellite to scan the planet, obtaining geographical information about the land.
- Precision agriculture is a type of farming management that utilizes remote sensing to measure variables in crops for decision making.
- In this case, we will focus on the production of corn stover, a fundamental agricultural by-product of corn harvests.
- We chose corn stover because it was difficult for farmers to know how much material they should extract, thus hindering their ability to maximize their profits.
- In previous studies, people have utilized remote sensing technology to measure pit, organic matter, etc. to identify corn stover.
- Hyperspectral sensors typically measure about 100 to 200 spectral bands of 5-30 nm bandwidths along a continuous electromagnetic spectrum.
- Using their canopy reflectance, we could determine the biophysical properties of the stover.

This study has two intentions:
1. Use image processing algorithms to identify corn stover in pictures taken by a handheld camera.
2. Using remote sensing technology, a specific waveband will be found using hyperspectral cameras that can differentiate corn stover from other materials such as soil.

Methods and Materials

Remote sensing:

- The remote sensing setup that will be used is a hyperspectral camera attached to a propeller plane.
- Aerial images of field crops will be operated through Parge, ENVI and ArcMap.
  - Parge will process the images through raster pixel data.
  - Wavelength of the pixels will be identified in ENVI.

Image processing:

- 30 randomly 1x1 meter plots of corn stover will be selected at 1879 T Ave South Amana, IA 52234, a corn farm near the University.
- Pictures of the plots will be taken using a handheld camera.
- Using a software called ERDAS Imagine, an algorithm using the RGB values of the selected plots will be derived to identify the presence of corn stover in the pictures.

Results

- By using image processing algorithms, we were able to determine a fairly accurate algorithm to identify both corn stover and vegetation by studying and placing restrictions on the RGB values of the photos.
- Algorithms used:(simplified for presentation purposes):
  - Vegetation:
    If [Green/(Red+0.1)>1.2] or [Red+Green<Blue and Red+Green<270]
  - Stover:
    If [Red+Green+Blue<570] and [Red-Green<30] or [Red-Green<15 and Green-Blue<15 and 60<Green<120]

Conclusions

1. Primary data of raw material aerial images were collected from the Hawkeye hyperspectral push broom sensor of an A-series sensor of 400-1000nm and an X-series sensor of 900-1700nm. Soil and stover reflectance were measured using a handheld near infrared spectrometer. Finally, a DEM file of the study site was collected from LiDAR data (see figure 5).
2. The key to the best image processing algorithm happened to be through the use of ratios. This is the solution to the problem with shadows potentially darkening the image, because when shadows shine over corn stover, the RGB values of the image decrease by a uniform and linear amount.
3. Corn stover and soil have a noticeable difference in reflectance indices, which could be used to differentiate stover from its surrounding material in an agricultural field. Furthermore, it was discovered that based on raw data, a change in carotenoids from stover could be the cause of the band difference.

Future Directions

- Hyperspectral data is still being processed at the moment to identify band differences.
- Image recognition for stover and vegetation could be improved by integrating more advanced computer vision techniques such as machine learning.
- Once a unique band is identified, models to detect the presence of corn stover can enhance precision agricultural methods increasing profit for farmers and producing agrarian surpluses.

References


Acknowledgements

Thanks to everyone in the REU program and anyone that has aided me in this wonderful opportunity. Special thanks to Pierre Yan, Siyong Huang, Richard Deng, Benjamin Hong, and Viktor Xu. Extra jumbo special thanks to Dr. Mark Linderman, Dr. Caglar Koylu and December Weir.
Seizure-free, but amnesic: Changes in verbal learning performance following anterior temporal lobe resection

Carolina Deifelt Streese, Jacob Wu, Kenneth Manzel, Daniel Tranel
Department of Neurology, University of Iowa

Introduction
Temporal lobe epilepsy (TLE) is drug-resistant in 30% of the cases. For some, temporal lobe resection (TLR) surgery is the only way to treat seizures1. Even so, surgery is successful in eliminating seizures only 50–60% of the times and reduces seizure frequency in another 20–30% of the cases2. Meanwhile, 60% of left TLR and 30% of right TLR surgery cases resulted in verbal memory declines3, an unintended complication that is the focus of our research project.

Hypothesis
To investigate the effect of laterality (left/right) on post-surgical memory decline, we investigated the following claims:
(1) Left (but not right) TLR patients will see significant verbal memory loss after surgery
(2) The shape of the learning curve for all groups will be logarithmically concave down

Method
Rey-AVLT was analyzed because it specifically measures verbal memory, revealing trial-trial improvements. Trial 1 (T1) of the Rey-AVLT reveals the patient’s initial memory, whereas Trial 5 (T5) is assumed to be indicative of their peak performance.

Results
We found an effect of laterality on T5 but not T1, and an effect of pre/post period on T1 but not T5. We found no interaction between laterality and pre/post period on T1/T5 score.

The shape of the learning curve was unexpectedly different for left vs. right (t(244.44) = 4.207, p < .001). Unlike the linear curve for left-sided patients, right TLE patients showed concave downward growth in learning curve as we predicted.

Similarly, left-sided vs. right-sided cases had different initial growth rate (T2-T1), with left acquiring .88 fewer words than right (t(280.42) = -4.58, p < .001).

Conclusion
• Concerns for aggravated memory loss should affect not only left TLR surgeries, as both groups are susceptible to declines
• It is possible that while both hemispheres contribute differentially to verbal memory, their interconnectedness requires the integrity of both for optimal performance
• It takes longer for left TLR patients to reach the same memory performance, so specific post-surgical intervention may focus on repetition and extended exposure

Acknowledgements
I am genuinely grateful to Carolina Deifelt Streese, Kenneth Manzel, and Dr. Daniel Tranel for their eager support and guidance throughout research.
Introduction

- **Bluetongue Virus (BTV)** is a well-documented virus that concerns farmers due to leading to mortalities primarily affecting sheep and livestock; wildlife can act as carriers as well[1].
- BTV is a double-stranded (ds) RNA virus of the family Reoviridae, genus Orvirivirus[1]—this is of particular interest due to the rarity of dsRNA genomes, even among animal viruses. Gaining a greater understanding of the BTV genome teaches us about the evolution of organisms with similarly structured dsRNA genomes.
- The BTV genome consists of 10 linear segments ranging from 822 to 3954 base pairs, coding for 7 structural proteins and 3 nonstructural proteins[2].
- BTV segment 2 serotype 1 (BTV-1) is the focus of study. We will estimate the mean evolutionary rate and geographic origin for BTV-1 using segment 2 sequences.
- Implication is in understanding the history of BTV and how it has evolved, moved, and changed over time.

Methodology

Samples of BTV were collected from open access NIH genetic sequence database Genbank with the documentation of locus name, year of sampling, and geographic location. They were run through ClustalX and then manually aligned on Sepronin in order to distinguish the difference in base pair substitutions. Aligned segments’ genome samples were run through BEAST for Bayesian analysis using the Markov chain Monte Carlo (MCMC) method to estimate the posterior distributions of the evolutionary rate and geographic origin. Corresponding locus name and dates were stochastically reassigned through R Studio Cloud and individually analysed with BEAST. The resulting randomized rate estimates provided a null distribution to which the original rate estimate was compared to determine our confidence in the rate estimate. The migration rates of BTV inferred in our phylogenetic analysis were assessed by calculating the Bayes factor for each, which provides an odds ratio for the presence of the rate.

Results

![Phylogenetic tree depicting evolutionary connection of BTV-1 samples and location](image1)

Fig. 1: Phylogenetic tree depicting evolutionary connection of BTV-1 samples and location

![Upper half of table depicting Bayes Factors of phyogeographic sampling locations rates. Lower half depicting supported migration rates (BF > 3).](image2)

Fig. 2: Upper half of table depicting Bayes Factors of phyogeographic sampling locations rates. Lower half depicting supported migration rates (BF > 3).

![Plot of empirical evolutionary rate estimate for BTV (column 1) in comparison to 20 randomized BTV rate estimates (columns 2-21). Note the empirical rate estimate does not overlap with the randomize rate estimates.](image3)

Fig. 3. Plot of empirical evolutionary rate estimate for BTV (column 1) in comparison to 20 randomized BTV rate estimates (columns 2-21). Note the empirical rate estimate does not overlap with the randomize rate estimates.

Conclusion

The evolutionary mean rate of Bluetongue Virus segment 2 serotype 1 (BTV-1) was estimated to be 2.63 x 10^5 substitutions per site, per year. It was determined to be statistically significant after falling outside of the error bars of the upper and lower bounds of higher posterior density (HPD) interval of 95% of the sampled values (Fig. 3). We can compare this estimate to a study performed by Carpi et al. (2010), who found "that Seg 2, -3, -6, and -10 evaluate at mean rates of between 0.52 and 6.9 x 10^4 substitutions per site, per year"[10], allowing us to postulate that our conclusion is reasonable as it is within the range of the findings set by this previous study.

From our phylogenographic analysis and calculations, 19 of our migration rates between sampling locations were well-supported by Bayes factors that were greater than our critical value of 3.0 (Fig. 2) - DZ-T (1.53), DZ-MA (1.28), DZ-TN (1.14), AU-CN (0.89), CM-ZA (0.94), CN-GR (0.95), CN-IN (0.93), CN-ZA (0.96), CN-KR (0.96), FR-ES (1.68), FR-US (0.95), GI-ES (1.03), GR-IN (0.78), GR-KR (0.94), IT-MA (1.29), IT-TN (1.31), PT-ES (1.02), ZA-SD (0.91), and KR-SD (1.01). As a result of the BEAST analyses, Figure 1 displays the evolutionary relations between BTV-1 samples collected based on date and location of sampling. From this, it can be concluded that the origin of BTV-1 is in South Africa (ZA). This study will be further developed and continued following this portion of the project through the similar data collection and analyses of the other BTV segments -1, -2, -3, -4, -5, -6, -7, -8, -9, -10, and the other serotypes, to determine their respective evolutionary rates and geographic origins. One outstanding question concerns cross-serotype variation in BTV origins and history of dispersal with implications for future policy regarding vaccination campaigns and prevention of bluetongue disease in livestock.

Data

- Alignment
- Analysis and Resampling

Acknowledgements

I am grateful for Dr. Drew Kitchen and his dependable guidance. I would also like to express thanks to Alex and Ishma, the iSTP program, and the 2019 iSTP cohort for the help and support in my project.

References

Cyclic Voltammetry (CV) Scans for HER

Results

<table>
<thead>
<tr>
<th>Film Composition</th>
<th>Average Measured Capacitance (microfarads)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nafion</td>
<td>5.2 ± 0.5</td>
</tr>
<tr>
<td>20:1 Nafion to carbon black (by mass)</td>
<td>180 ± 10</td>
</tr>
<tr>
<td>10:1 Nafion to carbon black (by mass)</td>
<td>470 ± 43</td>
</tr>
<tr>
<td>8 micron Spherotech magnetic particles</td>
<td>4.5 ± 0.4</td>
</tr>
<tr>
<td>1 micron Spherotech magnetic particles (film thickness doubled)</td>
<td>9 ± 1</td>
</tr>
</tbody>
</table>

Magnetic particles do not increase the capacitance of the electrochemical double layer.

As expected, increasing the concentration of carbon black in the film increases the capacitance.

Objectives:

1. Find optimal concentration of carbon black in the film.
2. Determine how capacitance is affected by the presence of magnetic particles.

Background

Hydrogen fuel cells are a way of storing energy from renewable and intermittent energy sources. The hydrogen evolution reaction (HER) drives energy storage and transfer, and the best electrode used is the platinum electrode. The use of platinum is too expensive for large scale energy purposes, so we are attempting to recreate capacitance and current by applying Nafion, magnetic particles, and carbon black mixtures as films on glassy carbon electrodes.

Part 1 key words: Hydrogen evolution, carbon black, magnetic particles, capacitance

References


Part 2 key words: Co(bpy)$_3^{2+}$, Square Wave Voltammetry, Magnetic Particles

Results

Glassy carbon electrodes could also be used as the positive electrode in batteries. Past studies have shown that the current signal from other types of electrodes is enhanced when magnetic film is applied, and we want to see if the same result applies to glassy carbon electrodes.

Objectives:

1. Observe effect of magnetic particles
2. Optimize film

Hypothesis: Magnetic particles enhance the current response of glassy carbon electrodes.

Implications

1. Higher concentrations of magnetic particles lead to higher current.
2. However, if there are too many particles, current signal decreases.

Part 2 key words: Co(bpy)$_3^{2+}$, Square Wave Voltammetry, Magnetic Particles

References


Methods

Cyclic Voltammetry (CV) Scans for HER

Applying different film to each electrode, set up cell in 0.5M H$_2$SO$_4$

Run scans at these scan rates for each electrode

Results Table 1: Capacitance Measurements of Each Film

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Methods

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Acknowledgements

Thank you Josh, Christian, Dr. Leddy, and the other members of the Leddy Lab for all your help and support along the way. Thank you Belin Blank Center and the SSTP Program for making this opportunity possible, and to the Army Research Office for sponsoring the work.

Methods

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References


Methods

Cyclic Voltammetry (CV) Scans for HER

Applying different film to each electrode, set up cell in 0.5M H$_2$SO$_4$

Run scans at these scan rates for each electrode

Figure 1. Cyclic voltammetry scans at different scan rates using electrode coated with 10:1 Nafion to carbon black film (Trial 1)

Figure 2. Currents at 0.5 V for different scan rates, where the capacitance value is the slope of the best fit line for 10:1 Nafion to carbon black film (Trial 1)

Figure 3. Model of the electrochemical double layer. Free charged particles in the solution are attracted to the electrode, and the distance between two oppositely charged layers form a capacitor (we measured this capacitance in part 1) (Adapted from Bard & Faulkner)

Figure 4. Wave forms in SWV (Adapted from Ramaley et al.)

While the double layer is forming, movement of charged particles creates a charging current, which interferes with the measured current. The smaller the change in voltage, the less time the formation of the double layer takes, and the effect of the charging current diminishes. Using SWV means that instead of a continuous increase in potential, potential would be changed in a staircase-like fashion.

Figure 5. The blue lines represent scans where the film resulted in a higher current signal than pure Nafion film, and the red lines represent films that resulted in lower current values than pure Nafion. A moderate amount of microparticles with 10 microliters of film applied (as opposed to 5 microliters for the other films) resulted in the highest current signal.

Figure 6. The slope of the lines can be used to calculate the diffusion coefficient. The magnetic film yielded a higher diffusion coefficient, which is consistent with the higher current values.
Exploring genetic interactions between a neurodegeneration mutant and Alzheimer’s disease in flies.

Pierre Yan¹; Richard Deng²; Krishna Madhav Nukala³; Anthony Lilienthal³; Alexander G. Bassuk, MD, PhD³; J. Robert Manak Ph.D³

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Introduction

Alzheimer’s disease is a widespread disease that affects 1 in 10 people over the age of 65¹. The onset of the disease has been associated with the incorrect processing of the APP gene in humans. This results in a build up of β-amyloid plaques in the brain². The fly ortholog, appl, has been shown to genetically interact with members of the Planar Cell Polarity (PCP) complex (Figure 1b). More specifically, Van gogh (Vang) interacts with appl with respect to neural connectivity in the Drosophila brain. Another member of the PCP complex, prickle, is known to genetically interact with Vang. We have recently shown that mutants of one isoform of prickle (prickle-prickle, or pk¹⁰) exhibit increased neurodegeneration, and we have demonstrated a genetic interaction between pk¹⁰ and appl with regard to adult survivability. We thus sought to determine whether the pk¹⁰ isoform interacts with appl regarding neuronal connectivity, a known role for pk¹⁰.

Hypothesis

Given that both appl and pk mutants have been shown to yield neuronal connectivity defects, we hypothesize that these mutants will show a genetic interaction with regard to embryonic neuronal connectivity.

Method

1. Fly lines assayed in this experiment: w¹¹¹⁸ (+/+), appl¹⁰, pk¹⁰ (pk), and appl¹⁰, pk.
2. Collect the 14 - 16 hour aged embryos from the various lines and remove the chorion membrane.
3. Fix the embryos in a 50/50 heptane and methanol mixture.
4. Remove the vitelline membrane by vigorously shaking the embryos in methanol.
5. Wash the embryos and perform immunohistochemistry (IHC) to stain the peripheral and motor neurons with antibodies (22C10 is a marker for peripheral neurons and Fasciculin II is a marker for motor neurons).
6. Image the embryos using confocal microscopy and quantify the number of defects in each line.

Results

<table>
<thead>
<tr>
<th></th>
<th>22C10</th>
<th>Fasciculin II</th>
<th>Total Counts</th>
</tr>
</thead>
<tbody>
<tr>
<td>+/+</td>
<td>70</td>
<td>38</td>
<td>108</td>
</tr>
<tr>
<td>appl¹⁰/appl¹⁰</td>
<td>56</td>
<td>50</td>
<td>106</td>
</tr>
<tr>
<td>pk/pk</td>
<td>50</td>
<td>57</td>
<td>107</td>
</tr>
<tr>
<td>appl¹⁰/appl¹⁰;pk/pk</td>
<td>8</td>
<td>0</td>
<td>8</td>
</tr>
</tbody>
</table>

Preliminary Results

Wildtype

Defect

Figure 2. Staining of PNS and motor neurons using 22C10 and fas2 primary antibodies with Alexa Fluor 488 secondary antibodies.

Figure 3. IHC of Drosophila embryos showing normal neuronal connectivity. All the embryos are stained with the antibody 22C10. Brightness and contrast are modified for ease of viewing.

Figure 4. Image the embryos using confocal microscopy and quantify the number of defects in each line.

Conclusions

- No wiring defects were found in any of the lines: +/+, appl¹⁰, pk, and appl¹⁰, pk
- This could be due to the fact that the sample size of each of the lines had low counts with low statistical power.
- There is also a possibility that there is no genetic interaction between pk and appl despite the interaction with the PCP complex members.
- Alternatively, the phenotype of these mutants may be revealed at later developmental stages.

Future Directions

- Increase total numbers for each of the lines to increase statistical power.
- Improve the method to increase the amount of useable embryos to be imaged.

References


Contact

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Combined Electrodialysis-Electrolysis Process for Nitrate Removal and Reduction

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\textit{Adlai E. Stevenson High School}\textsuperscript{1}; \textit{Secondary Student Training Program}\textsuperscript{2}; \textit{Department of Chemical and Biochemical Engineering, University of Iowa}\textsuperscript{3}

## Introduction
- High Nitrate/Nitrite levels threaten human health & infants
- Safe limit: 10mg/L (as N)
- Fertilizer $\rightarrow$ groundwater runoff
- Current methods do not remove N\textsubscript{2} or are energy inefficient

## Goal
- Combined electrolysiselectrodialysis setup

## Methods
**Part 1:**
- Existing ED setup
- Ran at constant voltage
- Determined using limiting current density

**Part 2:**
- Deposition using potentiostat
- Reticulated vitreous carbon
- Constant voltage applied

## Part 1: Electrodialysis
- Applied current: for ____
- Decreased conductivity lower nitrate concentration
- Carbon foam electrode was more energy efficient, and took less time to remove nitrate

## Part 2: Electrolysis

## Conclusions
- ED is possible using existing setup for nitrate removal
- Clear nitrate reduction using Pd/Cu
- Acidic conditions nonideal due to competing H\textsubscript{2} evolution

## Future Work
- Study impact of pH
- Deposit nanoparticles $\rightarrow$ reduce Pd
- Determine if catalyst is most cost effective
- Combine 2 components with RED
- Evaluate efficiency, calculate cost vs existing methods

## Acknowledgements
Many thanks to the following people: Sattar ALADI for mentoring me during SSTP, Dr. Syed Mubeen for providing invaluable advice, the Mubeen Research Group, the 2018 SSTP cohort, the University of Iowa, and the Belin-Blank Center
Heat stress alters mitochondria distribution and structure in cultured *Drosophila* giant neurons

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**Introduction**

**Why Drosophila?** (Hales, 2015)
- Fruit flies have a small genome with four chromosomes
- Easily cultured in lab, many offspring
- Short reproductive cycle of 9 to 10 days at 25 °C

**Mitochondrial Fission and Fusion**
- Mitochondria play a critical role in acclimatizing cells to metabolic or environmental stressors (Youle & van der Bliek, 2012).
- Mitochondrial fusion acts to reduce cellular stressors by combining the contents of multiple partially damaged mitochondria to form functional mitochondria (Youle & van der Bliek, 2012).
- Fission primarily functions to create new mitochondria while removing damaged mitochondria from the cell (van der Bliek, Shen & Kawajiri, 2013)
- Mutations in fusion and fission proteins are connected with numerous diseases, such as Parkinson’s, Alzheimer’s, and Huntington’s (Cho, 2010; Costa, 2010; Lutz, 2009; Shirendeb, 2012; Song, 2011; Wang, 2009)

**Methods**

Goal: Acquire different genotypes of UAS-mito-roGFP giant neurons for analysis. UAS-mito-roGFP is a genetically encoded tag for mitochondria. It is a UAS construct driven in subpopulations of neurons by the Gal4/UAS system.

1) Collect and plate *Drosophila* embryos from crossed females and males
2) Incubate some of the cultures for each genotype at 25 °C and the others at 29 °C
3) Image neurons across multiple days under phase-contrast and fluorescence, with a focus on neurite mitochondria
4) Measure a long, short, and representative length mitochondria for every visible neuron
5) Observe and graph differences in mitochondria structure and distribution under temperature and aging effects

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**How does heat stress effect mitochondria distribution and structure? Do different neuron classes possess different mitochondrial morphologies?**

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**Results**

- Mitochondria of cultures at 25 °C exhibited increased elongation, while those at 29 °C displayed punctate characteristics.
- As cultures become older, mitochondria median length begins to decrease.
- Mitochondria in neurons expressing *nsyb-Gal4* possessed the greatest median length.
- Mitochondria in neurons expressing *OK371-Gal4* had the greatest median length under heat stress.
- Neurons expressing *TH-Gal4* demonstrated the most punctuated characteristics at both 25 °C and 29 °C.

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**Conclusions**

Our results demonstrate a clear effect of heat and age stress on mitochondrial morphology.
- The consistent pattern of punctated mitochondria at 29°C and elongated mitochondria at 25°C exemplifies the effect of heat stress
- In high stress environments decreased fusion and increased fission occur in conjunction as an adaptive response, while the opposite occurs under levels of low stress (van der Bliek, 2013)
- Consistent increase in median length of mitochondria from zero to six days demonstrate a period of growth.
- A considerable decrease in median length at thirteen and fifteen days demonstrate the effect of age stress

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**Future implications**

- Further understanding of the specific reactions of mitochondria to stress could aid in development of treatments for mitochondrial and neurodegenerative diseases
- Inhibition of mitochondrial division may result in disease-associated phenotypes of multiple neurodegenerative diseases

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**References**


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**Acknowledgements**

I would like to thank Dr. Wu and the other lab members for advising and supporting me throughout these five weeks
Large-scale CanaryTrap implementation: Detecting data misuse by Facebook’s third-party apps
Kathy Zhong1, Shehroz Farooqi2, Zubair Shafiq2
Amador Valley High School1, Department of Computer Science, The University of Iowa2

Introduction and Background

Online social networks offer their users the ability to access other applications more conveniently through their interfaces. Facebook, for example, offers users millions of apps to log in via Facebook account.

Problem

Third-party applications ask for a multitude of information to enhance user experience. However, many of these apps are often easily breached or misuse information themselves. There have already been multiple instances of misuse of data illicitly collected via third-party applications, such as the Cambridge Analytica scandal.

The danger such threats pose increases with consideration of the fact that research has found that third-party applications tend to ask for and store more information than is considered strictly necessary (Huber et al., 2013), and are often under attack by collusion networks and other cybercriminals hoping to manipulate users’ accounts (Farooqi et al., 2017).

Solution: CanaryTrap

CanaryTrap is an approach that can be used to systematically monitor the way apps are using private information by leaking honeypots, in this case email addresses, and then monitoring the emails those accounts receive. We analyze received emails to detect the misuse of user’s data by third-party applications.

Key Contributions

- Facebook’s anti-abuse systems make audit by independent watchdogs, including large-scale CanaryTrap implementation, difficult
- Create a large number of accounts to run multiple instances of experiments
- Make accounts as realistic as possible
- Initiation of a long-term implementation of CanaryTrap over thousands of third-party apps on Facebook
  - To mimic human behavior, CanaryTrap processes around ten apps every three hours
  - Some apps begin illicitly spreading data immediately, while others do so gradually
  - Transition to matrix implementation of CanaryTrap
- Blackbox experimentation and analysis of Facebook’s anti-abuse systems
  - Facebook looks at device activity as well as account activity
  - Factors include account creation rate, post rate, and email rotation rate

Method

Honeypot: a small piece of information purposely leaked to be monitored to detect its misuse
- Create Facebook accounts on different IP addresses; each one serves as a different instance
- Manual creation process to prevent being locked out by Facebook’s anti-abuse systems
- For each instance: change the account’s primary email address, install an app, then uninstall it, before repeating the process
  - This way, we have a 1:1 mapping between email address and third-party app
  - This process is automated, using Selenium
- Analyze the emails received and categorize them as recognized (sent by the respective app installed with that email as the primary address) or misuse (sent by an app not related to the installed app)
  - We manually further inspect misuse categorizations to avoid false positives

Results

- Facebook Account Creation
  - Number Of Accounts
  - Failed Account Creation
  - Succeed Account Creation Status
- Post-Account Creation
  - Email Confirmation Unsuccessful
  - Account Locked
  - Experiment Initiated
  - Facebook locks some accounts directly if they were created too quickly
  - More consistent activity on an account makes it less likely to be locked

Email Analysis

- Date
  - Failed Account Creation
  - Succeed Account Creation Status
  - Email Confirmation Unsuccessful
  - Account Locked
  - Experiment Initiated

Future Directions

- Continue implementing CanaryTrap for all third-party apps on Facebook
  - Adjust to matrix implementation to maximize scalability and minimize error
  - Expand CanaryTrap to monitor apps on other platforms
  - Develop a website to inform the public of apps that are misusing their data
  - Further research into Facebook’s anti-autimation policies and practices

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Special thanks to Dr. Zubair Shafiq and Shehroz Farooqi for their guidance over these past weeks for this project, as well as to the Secondary Student Training Program and Belin-Blank Center for this opportunity.

References


Matrix Implementation

To maximize scalability of the experiment, we can implement a matrix implementation; essentially, a multi-dimensional version of the current array implementation.

If honeypots HT A1 and HT B1 receive the same email from the same sender, we can, under the assumption that an app will send promotional emails to all emails, trace that email back to AppX.

Limitation: as we decrease the number of honeypots used, we increase probability of false positives due to the arrangement of the matrix and method of corresponding emails to apps
If app1 and app2 send emails from the same email, for example, there is a possibility that that will be recorded as app1 and app2. This probability of getting a false positive increases as the number of Facebook accounts (and thus “dimensions”) used increases, but decreases as the number of honeypots increases.

For a matrix implementation with two Facebook accounts, with m and n honeypots, respectively, we can model the probability of getting a false positive with

\[
\text{err} = \frac{n}{(m + n) + (m + 1)}
\]

where \( \text{err} \) is the probability that one pair of apps send the same email.