CONCORDIA UNIVERSITY OF EDMONTON
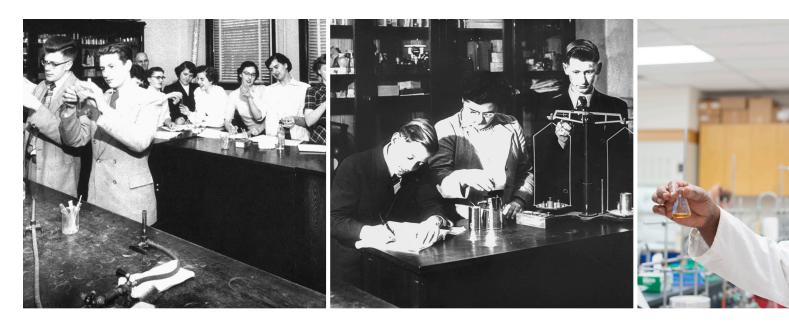
CONCORDIA 100
1921 – 2021

URSCA 2021
VIRTUAL EDITION
MAY 3–4,2021

Undergraduate Research Under
Extraordinary Circumstances

Undergraduate Research Under Extraordinary Circumstances

CONTENTS

Welcome to URSCA

Concordia University of Edmonton (CUE) is proud to be the 2021 host of the 7th Annual Undergraduate Research in Science Conference of Alberta. This conference provides a much-needed avenue for talented undergraduate scientists throughout Alberta to present their research work for scrutiny and dissemination. In doing so it serves to highlight the value that undergraduate research brings to the various scientific disciplines on display at the conference, and provides an important learning opportunity not only for the researchers and presenters, but also the attendees.

Hosting the URSCA this year at CUE is fitting because it coincides with our 100th anniversary, and we are currently engaged in a year-long celebration of who we were, who we are, and where we are headed. Like post-secondary institutions throughout Alberta, we have a long and distinguished history of producing exceptional undergraduate scientists, many of whom have gone on to make significant contributions in science and medicine in their subsequent careers.

The theme of the conference this year is, very appropriately, "Undergraduate Research under Extraordinary Circumstances". The scientists who are presenting their work this year have had to grapple with the additional challenges of conducting scientific work during a pandemic. This has doubtlessly informed their research and become part of the story of their own development as researchers. Difficulties breed resilience, and it is a testament to the

perseverance of these undergraduate researchers that they were able to complete their projects and present them over the next couple of days.

Just as the research being presented at this year's URSCA was conducted under trying circumstances, so too is the conference. Vaccines have yet to be fully rolled out in Canada, and so our conference has, like so many before it, been forced online. This has raised additional challenges for the organizers who are to be thanked for their hard work and dedication for bringing this conference to fruition.

Wishing you much enjoyment as you celebrate undergraduate science research at this year's URSCA.

Tim Loreman

ALEJANDRO ADEM

KEYNOTE SPEAKER

A New World of Possibilities for Canadian Undergraduates

Professor Alejandro Adem was appointed president of the Natural Sciences and Engineering Research Council of Canada (NSERC) in October 2019.

As a highly accomplished researcher in the field of mathematics and a faculty member at the University of British Columbia, Professor Adem has significant leadership experience in the research and innovation ecosystem. Before joining NSERC, he was Chief Executive Officer and Scientific Director of Mitacs.

As CEO of Mitacs, Professor Adem oversaw an unprecedented expansion of its programs, with the goal of delivering 10,000 research-based internships annually across Canada and abroad. He worked closely with stakeholders to launch the Mitacs Canadian Science Policy Fellowship in 2016, which places talented academics in science policy roles in both federal and provincial governments. Other important milestones under his leadership include an Indigenous engagement initiative, an innovative entrepreneurship program, and a number of global mobility agreements with partner countries across the world. Professor Adem obtained his PhD at Princeton University and has authored over 70 articles as well as two books, delivered over 360 invited research lectures around the world, and has held post-doctoral or visiting positions at Stanford University, the Institute for Advanced Study in Princeton, the ETH-Zurich, the Max Planck Institute in Bonn, the University of Paris VII and XIII, and Princeton University. His distinctions include a Sloan Doctoral Dissertation Fellowship (1985), a USA National Science Foundation Young Investigator Award (1992), Romnes Faculty Fellowship (Wisconsin Alumni Research Foundation, 1995), a Vilas Associate Award (University of Wisconsin, 2003), Canada Research Chair at UBC (2004), Fellow of the American Mathematical Society (2012), Ten Most Influential Hispanic Canadians (2015), the Canadian Mathematical Society's Jeffery Williams

"As the global pandemic continues to expose deep societal challenges and create a sense of uncertainty about the future, there has never been a greater need for the talent and ingenuity found in our research community. With NSERC's support, a new generation of young researchers are seizing the opportunity to re-think how we live in our brave new world."

Prize (2015), and Corresponding Member of the Mexican Academy of Sciences (2017). Professor Adem served as Director (2008-2014) and Deputy Director (2005-2008) of the Pacific Institute for the Mathematical Sciences. From 1989 to 2004 he was a faculty member at the University of Wisconsin-Madison (USA).

Professor Adem has served on a variety of scientific, editorial, and governance boards for the worldwide mathematical sciences community, including the Advisory Board for the Association for Women in Mathematics and the International Mathematical Union's Committee for Women in Mathematics.

Conference at a Glance

Please note: All General Sessions are denoted by an asterisk (*) and share the meeting ID of: 901 158 8300.

MONDAY MAY 3, 2021

*2:00 - 2:15 pm............................ **Welcome Message from Dr. Tim Loreman,** President and Vice-Chancellor, Concordia University of Edmonton
Emcee: Dr. Ramses Ilarraza, Asst. Vice-President Research, Concordia University of Edmonton

*2:15 - 2:30 pm............................ **CUE 100 Anniversary Video**

*2:30 - 3:15 pm............................ **Keynote Speaker Presentation by Dr. Alejandro Adem**, President, Natural Sciences and Engineering Research Council of Canada

3:15 - 3:30 pm............................ **Break**

3:30 - 6:30 pm............................ **Oral Presentations (Session A)**

*6:30 - 8:00 pm............................ **Networking**

TUESDAY MAY 4, 2021

*8:30 - 9:00 am............................ **Opening Remarks from Dr. Valerie Henitiuk**, Vice-President Academic and Provost, Concordia University of Edmonton
Emcee: Dr. Patrick Kamau, Dean of Science and Acting Dean of Graduate Studies, Concordia University of Edmonton

9:00 - 9:15 am............................ **Break**

9:15 - 12:00 pm............................ **Oral Presentations (Session B)**

12:00 - 1:00 pm............................ **Lunch Break**

*1:00 - 1:15 pm............................ **Imagination to Innovation: Presentation by Student Entrepreneur, Korah Anderson**

1:15 - 1:30 pm............................ **Break**

1:30 - 4:30 pm............................ **Oral Presentations (Session C)**

4:30 - 6:00 pm............................ **Break**

*6:00 - 7:00 pm............................ **Awards Ceremony**

Oral Presentation Schedule

SESSION A1 | MEETING ID: 943 1213 4759

3:30 p.m.
VANESSA BOONE (Ambrose University)
CONSTRAINTS ON CYTOCHROME C OXIDASE I
EVOLUTION IN FISH

3:45 p.m.
COLE HARTUNG (Ambrose University)
VARIATION OF THE COI GENE IN FISH

4:00 p.m.
FULNOOR CHEEMA (Concordia University of Edmonton)
DETERMINING THE EFFECTS OF ANTIMICROBIAL
PEPTIDE HUMAN B-DEFENSIN 2 ON
STAPHYLOCOCCUS EPIDERMIDIS BIOFILM
INHIBITION

4:15 p.m.
ALISHIA PECORILLI (Concordia University of Edmonton)
THE EFFECTS OF DIHYDROERGOTAMINE ON THE
DEVELOPING CARDIOVASCULAR SYSTEM OF A
CHICK EMBRYO

4:30 p.m.
MORGAN VERCHOLUK (Concordia University of Edmonton)
ASSESSING THE INHIBITORY EFFECT OF
RETAPAMULIN ON ESCHERICHIA COLI (ATCC 13706)

4:45 p.m.
APSARA SRINIVAS (Lethbridge College)
PRAIRIE PLANT EXTRACTS THAT INCREASE THE
LAG PHASE OF BACTERIAL GROWTH. A POTENTIAL
SOLUTION FOR THE FOOD INDUSTRY TO REDUCE
FOOD SPOILAGE

5:00 p.m.
NOAH BROOKS (MacEwan University)
ISOLATION OF MICROSATELLITES FROM
CYPRIPEDIUM PASSERINUM BY FIASCO

5:15 p.m.
ETHAN HAGEN (MacEwan University)
THE EFFECTS OF REPEATED MICRODOSING WITH
LSD ON ZEBRAFISH (DANIO RERIO) BEHAVIOUR

5:30 p.m.
JOLIE HAMEL (MacEwan University)
SCREENING PHYTOCHEMICAL EXTRACTS OF
INVASIVE ALBERTAN WEEDS FOR ANTI-BIOFILM
PROPERTIES

5:45 p.m.
HAILEY PON (MacEwan University)
THE EFFECTS OF VARYING CONCENTRATIONS OF
HEMIN ON THE DIFFERENTIATION OF CHRONIC
MYELOID LEUKEMIA (CML) CELL LINE K562

Oral Presentation Schedule

3:30 p.m.
JENNIFER ROTH (MacEwan University)
WHAT CAN NORTHERN PIKE (ESOX LUCIUS) STOMACH CONTENTS REVEAL ABOUT POST-MANAGEMENT COMMUNITY DYNAMICS IN LAC LA BICHE, ALBERTA?

3:45 p.m.
SHIVANI SOLANKI (MacEwan University)
INVESTIGATION OF 30 DAYS OF EXPOSURE TO OIL SANDS PROCESS-AFFECTED WATER IN ZEBRAFISH (DANIO RERIO)

4:00 p.m.
BRITTANY SUPINA (MacEwan University)
ANTIMICROBIAL ACTIVITY OF PHYTOCHEMICALS EXTRACTED FROM ALBERTAN INVASIVE WEEDS

4:15 p.m.
BRITTANY WISEMAN (MacEwan University)
HUMAN CHRONIC MYELOGENOUS LEUKEMIA K562 CELLS UNDERGO ERYTHROCYTIC DIFFERENTIATION AND CELL CYCLE INTERRUPTION IN RESPONSE TO PMEA (9-(2-PHOSPHONYL-METHOXYETHYL)-ADENINE)

4:30 p.m.
BRITTANY WISEMAN (MacEwan University)
IDENTIFYING THE NUCLEAR LOCALIZATION SIGNAL OF THE ARABIDOPSIS TRANSCRIPTION FACTOR FLOWERING LOCUS C

4:45 p.m.
RASHIDA AAMIR (Mount Royal University)
EVALUATION OF MYOD GENE EXPRESSION IN C2C12 CELLS CULTURED ON EXTRACELLULAR MATRIX PROTEINS

5:00 p.m.
DANIEL MAJOR (Mount Royal University)
MYOGENIC DIFFERENTIATION INDUCED BY CELL-TO-CELL CONTACT VERSUS SERUM STARVATION: EFFECTS ON MYOD, MYOGENIN, AND MYOSIN HEAVY CHAIN MRNA EXPRESSION IN C2C12 CELLS

5:15 p.m.
LAURA REYES PALACIOS (Mount Royal University)
EFFECT OF GROWTH AND DIFFERENTIATION MEDIA ON MRNA EXPRESSION LEVELS OF M-CADHERIN AND MYOGENIN DURING MYOGENESIS OF C2C12 MYOBLAST CELLS

5:30 p.m.
AMARPREET SANGHA (Mount Royal University)
EXPRESSION OF RISK GENES LINKED TO VITAMIN D RECEPTOR SUPER ENHANCER REGIONS AND THEIR ASSOCIATION WITH PHENOTYPE SEVERITY IN MULTIPLE SCLEROSIS: PILOT STUDY

5:45 p.m.
KIARA O'SHEA (St. Mary's University)
SURVEY FOR MACROBIOTUS OCCIDENTALIS AND DIAFOROBIOTUS SPP. IN VICTORIA, BRITISH COLUMBIA, CANADA, AND FIRST IDENTIFICATION OF PARASCON SP. IN CANADA

Oral Presentation Schedule

3:30 p.m.
JARED VANDERZWAAG (Ambrose University)
SYNTHESIS AND EVALUATION OF ENVIRONMENTALLY FRIENDLY WOUND-CARE PRODUCTS—APPLICATION OF GREEN CHEMISTRY IN UNDERGRADUATE RESEARCH

3:45 p.m.
RAMANJOT KAUR (Concordia University of Edmonton)
QUANTIFICATION OF FRUCTOSE AND GLUCOSE BY HPLC-UV AND OZASONE DERIVATIZATION

4:00 p.m.
BRYCE KIRK (Concordia University of Edmonton)
SYNTHESIS OF HEPTA-1,3,6-TRIEN-5-OLS FOR POTENTIAL 8PI ELECTROCYCLIZATIONS

4:15 p.m.
MANDEEP SINGH (Concordia University of Edmonton)
ANALYTICAL METHOD DEVELOPMENT FOR HPLC QUANTITATION OF IBUPROFEN IN THREE PHARMACEUTICAL PRODUCTS

4:30 p.m.
THÉRÈSE WILSON-RAWLINS (Concordia University of Edmonton)
THE IMPACT OF PRO OXIDANT BIOMETALS ON NON-ENZYMATIC GLYCATION UNDER PHYSIOLOGICAL CONDITIONS

4:45 p.m.
RADHIKA SAINI (MacEwan University)
CHROMATOGRAPHIC AND NMR ANALYSIS OF ALBERTAN INVASIVE WEED SPECIES

5:00 p.m.
BHADRA PANDYA (University of Lethbridge)
QUANTUM MECHANICAL TREATMENT OF POST-TRANSCRIPTIONALLY MODIFIED URACIL BASE PAIRS

Oral Presentation Schedule

3:30 p.m.
CARLEY AQUIN (MacEwan University)
DO INCREMENTAL THEORIES OF WELL-BEING AND OTHER WELL-BEING BELIEFS PREDICT PROSOCIAL SPENDING?

3:45 p.m.
MIRAY HELMY (MacEwan University)
EMPATHY, SELF-AWARENESS AND PET-OWNERSHIP

4:00 p.m.
JADE RADKE (MacEwan University)
USING TAGTEACH TO INCREASE CREATIVE PLAY BEHAVIOR IN CHILDREN WITH AUTISM

4:15 p.m.
GODI JIBI (Mount Royal University)
THE SIGNIFICANCE OF HIGH ALTITUDE ACCLIMATIZATION ON THE HYPEROXIC VENTILATORY WITHDRAWAL TEST PERFORMED ON NATIVE LOWLANDERS

4:30 p.m.
ANTHONY MARULLO (Mount Royal University)
CEREBROVASCULAR RESPONSES DURING VOLUNTARY BREATH HOLDING ARE LARGER THAN REBREATHING

4:45 p.m.
DEXTER MERENICK (Mount Royal University)
NEUROVASCULAR COUPLING IS UNCHANGED DURING SITTING, STANDING OR WALKING: IMPLICATIONS FOR ACTIVE WORKSTATIONS

5:00 p.m.
TARA SALLOUM (Mount Royal University)
CEREBRAL BLOOD FLOW PULSATILITY INDEX IS UNCHANGED DURING SUPERIMPOSED LOWER-BODY NEGATIVE PRESSURE IN HEAD-UP TILT IN ANTERIOR AND POSTERIOR CEREBRAL CIRCULATIONS

5:15 p.m.
SARAH ALMAS (University of Alberta)
PREVENTION OF CEREBRAL PALSY DURING THE PRENATAL PERIOD

5:30 p.m.
BUSHRA ANJUM (University of Alberta)
ROLE OF SEX AND THE MICROBIOME IN PRODUCTION OF 'NATURAL' ANTIBODIES IN A MOUSE MODEL

5:45 p.m.
JESSICA BENNETT (University of Alberta)
UNDERSTANDING THE ROLE OF DDX1 EXPRESSION IN NEUROBLASTOMA RESPONSE TO TREATMENT

6:00 p.m.
MAI HUYNH (University of Alberta)
INVESTIGATING THE ROLE OF DEXAMETHASONE ON IMMUNE REGULATION

Oral Presentation Schedule

9:15 a.m.
ALANA LOUTAN (MacEwan University)
CHARACTERIZATION OF AN APTAMER FOR
AFLATOXIN B1 AND SUBSEQUENT APTASENSOR
DESIGN

9:30 a.m.
LARA FLANZBAUM (Mount Royal University)
GENOME MINING FOR THE DISCOVERY OF
CIRCULAR ANTIMICROBIAL PEPTIDES

9:45 a.m.
LEAH LUSSIER (Mount Royal University)
GENOME MINING AND ISOLATION OF BACTERIA-
DERIVED ANTIMICROBIALS

10:00 a.m.
LANA WONG (University of Calgary)
IDENTIFYING THE INTERACTIONS BETWEEN
SHEWANELLA-LIKE PROTEIN PHOSPHATASE 1, AND
ITS SPECIFIC SUBSTRATE, CALVIN CYCLE PROTEIN 12
IN ARABIDOPSIS THALIANA

10:15 a.m.
NIC JUJIHARA (University of Lethbridge)
BIOPHYSICAL AND STRUCTURAL
CHARACTERIZATION OF SP1-ZINC FINGER DOMAIN
AND HEPATITIS B VIRUS PROMOTER INTERACTION

10:30 a.m.
KIERAN MEADOWS (University of Lethbridge)
STUDYING TRNA BINDING AND MODIFICATION BY
THE ENZYME TRMB

10:45 a.m.
SEAN PARK (University of Lethbridge)
TOWARDS UNDERSTANDING FLAVIVIRAL GENOME
CYCLIZATION

11:00 a.m.
JULIA STROUD (University of Lethbridge)
LONGITUDINAL TIME-SERIES ANALYSIS OF THE
EFFECTS OF LONG-DURATION SPACE TRAVEL IN
MALE AND FEMALE NASA ASTRONAUTS USING A
1H-NMR-BASED METABOLOMICS APPROACH

11:15 a.m.
KATRINA TAYLOR (University of Lethbridge)
INVESTIGATING THE INTERACTION BETWEEN
PDCD4 AND EIF3F WITH RESPECT TO TRANSLATION
REGULATION

11:30 a.m.
SCOTT TERSTEEG (University of Lethbridge)
LEARNING WHAT IT TAKES TO BE ESSENTIAL IN
RIBOSOME SYNTHESIS: A MUTAGENESIS STUDY OF
SNR30 RNA FUNCTIONALITY

Oral Presentation Schedule

9:15 a.m.
EVAN BUIST (The King's University)
EFFECTS OF INTERANNUAL VARIABILITY IN
SEED PRODUCTION OF 5-NEEDLED PINES ON
NUTCRACKER CACHING IN BURNS

9:30 a.m.
DANIEL CLARK (The King's University)
ASYMMETRICAL BINDING OF HSP90
COCHAPERONES AND ITS EFFECTS ON
COCHAPERONE CYCLING

9:45 a.m.
JACK LACROIX (The King's University)
THE EFFECTS OF BETA-CYCLODEXTRIN ON
ZEBRAFISH LENS CLARITY

10:00 a.m.
EMILIE PORTER (The King's University)
ECHINOCOCCUS MULTILOCULARIS PREVALENCE
AND RISK FACTORS FOR INFECTION IN DOMESTIC
DOGS IN EDMONTON ALBERTA

10:15 a.m.
KAEGAN FINN (University of Alberta)
PARASITES AND STABLE ISOTOPES: THE POTENTIAL
FOR NEW TAXON-SPECIFIC DISCRIMINATION
FACTORS

10:30 a.m.
MATTHEW GERUN (University of Alberta)
THE MOLECULAR BASIC OF CAROTENOID
BIOSYNTHESIS IN CLEOMACEAE

10:45 a.m.
ROBERT LU (University of Alberta)
DISENTANGLING THE WORM: A POPULATION-LEVEL
GENETIC ASSESSMENT OF A SNAIL SYMBIONT

11:00 a.m.
PATRICIA ANN VILLARAMA (University of Alberta)
OLFACTORY IMPRINTING OF BETA-PHENETHYL
ALCOHOL IN ZEBRAFISH

11:15 a.m.
ANDREW WU (University of Alberta)
MAPPING CEREBRAL ABNORMALITIES USING
TEXTURE ANALYSIS IN ALS WITH T2-FLAIR MRI: A
MULTICENTER STUDY

11:30 a.m.
JULIA CASORSO (University of Calgary)
ASSESSING NATURAL SOURCES OF ETHANOL IN
WILD PRIMATE FOODS: TESTING KEY PREDICTIONS
OF THE DIETARY EXPOSURE HYPOTHESIS

Oral Presentation Schedule

TUESDAY MAY 4 | 9:15 AM - 12:00 PM

SESSION B3 | MEETING ID: 941 0121 3632

9:15 a.m.
JAYNA BERGMAN (University of Lethbridge)
THE IMPACT OF ASSUMPTIONS ABOUT PREVALENCE ON MODELS OF SUITABLE HABITAT FOR LONG-TOED SALAMANDERS IN SOUTH-WESTERN ALBERTA.

9:30 a.m.
CHLOE DEVOY (University of Lethbridge)
EFFECTS OF MATERNALLY DEPOSITED 1,2,5,6-TETRABROMOCYCLOOCTANE (TBCO) ON EARLY LIFE STAGE DEVELOPMENT AND REPRODUCTION IN JAPANESE MEDAKA (ORYZIAS LATIPES)

9:45 a.m.
LIAM GALVIN (University of Lethbridge)
LEARNING AND HAND USE IN CRICKET PREDATION BY THE MOUSE

10:00 a.m.
DANIEL GRANT (University of Lethbridge)
A NOVEL PIPELINE FOR METHANOGEN COMMUNITY ANALYSIS VIA ILLUMINA DNA SEQUENCING DATA

10:15 a.m.
NADIA HAND (University of Lethbridge)
INVESTIGATION OF A NOVEL "CLUMP" PHENOTYPE OBSERVED WITH STAPHYLOCOCCUS EPIDERMIDIS TREATED WITH PRAIRIE PLANT EXTRACTS

10:30 a.m.
MELISSA HICKLE (University of Lethbridge)
AN ANALYSIS OF FORKED-LIKE GENE EXPRESSION IN THE VASCULAR CAMBIUM DURING INDUCED SECONDARY GROWTH

10:45 a.m.
HUNTER JOHNSON (University of Lethbridge)
TOXICITY OF BENZOTRIAZOLE ULTRAVIOLET STABILIZERS (UV-P, UV-9, UV-090) TO EARLY LIFE STAGE DEVELOPMENT OF ZEBRAFISH (DANIO RERIO)

11:00 a.m.
CATRIONE LEE (University of Lethbridge)
FEEDLOTS TO SEWAGE: METAGENOMICS IN A ONE HEALTH APPROACH TO ANTIMICROBIAL RESISTANCE

Oral Presentation Schedule

9:15 a.m.
ALI BOUKRICH (Concordia University of Edmonton)
A UNIFIED VIEW OF EPIDEMIOLOGICAL AND ARTIFICIAL
INTELLIGENCE BASED MODELLING TO APPLY EMPIRICAL
EVIDENCES IN RATIONAL PUBLIC HEALTH POLICY
MEASURES

9:30 a.m.
JAINTH CHAUDHARY (Concordia University of Edmonton)
SAFE AI: PRIVACY PRESERVING MACHINE LEARNING
ALGORITHMS FOR TRUST SENSITIVE

9:45 a.m.
SHUBHAM MALHOTRA (Concordia University of Edmonton)
COVID-19 CHATBOT: A NATURAL LANGUAGE PROCESSING
AND ARTIFICIAL INTELLIGENCE POWERED

10:00 a.m.
SHUBHAMPREET SINGH (Concordia University of
Edmonton)
VIRTUAL COOK 2.0: A USER INTERACTIVE WEB BASED
SMART RECIPE SEARCH ENGINE IN FLASK

10:15 a.m.
ANGELA LI (Mount Royal University)
APPLICATION OF AN SVEIRD MODEL TO TRACK THE
SPREAD OF COVID-19 IN NIGERIA

Oral Presentation Schedule

9:15 a.m.
RAMESH MAHDAVIFAR (University of Alberta)
IMPACT OF CD36 MUTANT ON FATTY ACID UPTAKE

9:30 a.m.
TARANA (RIYA) MANGUKIA (University of Alberta)
ASSEMBLING AN ATOMIC MODEL OF THE HIV-1 VIRAL SPIKE ENVELOPE GLYCOPROTEIN: IMPLICATIONS FOR VIRAL ENTRY

9:45 a.m.
MUJTABA SIDDIQUE (University of Alberta)
ASSESSMENT OF ADHERENCE TO PERIOPERATIVE ANTICOAGULATION DISCONTINUATION GUIDELINES IN PATIENTS WITH ATRIAL FIBRILLATION AND PREVIOUS STROKE

10:00 a.m.
OJAS SRIVASTAVA (University of Alberta)
ANTI-VEGF SWITCH THERAPY IN RADIATION RETINOPATHY

10:15 a.m.
JENNY LE (University of Alberta)
CONTRIBUTIONS OF EXECUTIVE FUNCTION TO PARENTING

10:30 a.m.
EMMA MONAGHAN (University of Alberta)
AGAINST THE GRAIN: PROMOTING IDENTITY CONTINUITY AS A STRATEGY TO ELEVATE GROUP SUPPORT FOR CHANGE

10:45 a.m.
JULIANNA SVISHCHUK (University of Calgary)
INOCULUM EFFECTS IN STAPHYLOCOCCUS AUREUS ISOLATED FROM THE AIRWAYS OF INDIVIDUALS WITH CYSTIC FIBROSIS

11:00 a.m.
JESSICA ZHANG (University of Calgary)
WHAT NUTRITIONAL INTERVENTIONS EXIST FOR CANADIAN INDIGENOUS ADULTS? A SCOPING REVIEW

11:45 a.m.
KENNEDY LEWIS (University of Lethbridge)
THE EFFECTS OF PRECONCEPTION MATERNAL NICOTINE AND ALCOHOL ON ADULT OFFSPRING HIPPOCAMPAL VOLUME AND ASSOCIATED BEHAVIOR

Oral Presentation Schedule

9:15 a.m.
ANA MUCALICA (MacEwan University)
THE PHYSICAL NATURE OF THE ONE-DIMENSIONAL CUBIC NONLINEAR SCHRÖDINGER EQUATION

9:30 a.m.
KHOA BUI (Concordia University of Edmonton)
USING THE LLL-ALGORITHM TO BREAK THE RSA CRYPTOSYSTEM

9:45 a.m.
ANNA KLICK (MacEwan University)
IN ALL DIRECTIONS: HIGHER DIMENSIONAL ARITHMETIC PROGRESSIONS IN MEYER SETS

10:00 a.m.
ALI BOUKRICH (Concordia University of Edmonton)
USING THE LLL ALGORITHM IN ATTACKING KNAPSACK CRYPTOSYSTEMS

10:15 a.m.
JANNAH AIZON (MacEwan University)
MESSENGERS FROM THE ASTEROID BELT: A STUDY OF DIOGENITES NORTHWEST AFRICA 10268 AND 7464

10:30 a.m.
ASHLEY HICKEY (MacEwan University)
USING THREE-STATE ISING MODEL TO STUDY CANCER CELL RESPONSE TO CHEMOTHERAPEUTIC DRUGS

10:45 a.m.
LUISA VARGAS SUAREZ (University of Calgary)
NUCLEAR ENERGY FROM DIFFERENT PERSPECTIVES

11:00 a.m.
SNEHASIS ADDY (University of Calgary)
ERROR CORRECTION IN QUANTUM KEY DISTRIBUTION (QKD) USING LOW DENSITY PARITY CHECK (LDPC) CODES

11:15 a.m.
JOSHUA PELTONEN (University of Calgary)
THE 3D MORPHOLOGY OF MOLECULAR CLOUDS

Oral Presentation Schedule

1:30 p.m.
KIRSTY MCFADYEN (University of Lethbridge)
CHANGES IN THE ELEVATIONAL DISTRIBUTIONS OF
PLANT SPECIES IN WATERTON LAKES NATIONAL
PARK OVER 25 YEARS OF CLIMATE WARMING

1:45 p.m.
JHANVI MEHTA (University of Lethbridge)
THE BRAIN AND CANNABIS: INVESTIGATING THE
EFFECTS OF HIGH-CBD CANNABIS STRAINS ON
MOTOR RECOVERY FOLLOWING STROKE

2:00 p.m.
YAMIN RAZA (University of Lethbridge)
DETERMINING THE EFFECTS OF UV-STABILIZERS,
UV-9 AND UV-090, ON OOCYTE MATURATION IN
ZEBRAFISH (DANIO RERIO)

2:15 p.m.
JAXON REITER (University of Lethbridge)
GERMINATION TRIALS AND PHENOLOGICAL
ANALYSIS OF CANADA'S ENDANGERED WOOD
POPPY (STYLOPHORUM DIPHYLLUM)

2:30 p.m.
MELISSA TELFER (University of Lethbridge)
MORPHOLOGICAL AND MOLECULAR
IDENTIFICATION OF AIRBORNE FUNGAL SPORES IN
POTATO FIELDS OF ALBERTA

Oral Presentation Schedule

1:30 p.m.
ELS HRYNIW (Concordia University of Edmonton)
DETERMINATION OF BASELINE SOIL ORGANIC
MATTER AND 13C STABLE ISOTOPE PRIOR TO
BIOSOLIDS APPLICATION

1:45 p.m.
BEN MICHALCHUK (MacEwan University)
EVALUATING THE LATE PLEISTOCENE AND EARLY
HOLOCENE ARCHAEOLOGICAL POTENTIAL IN
WEST-CENTRAL ALBERTA: A GEOMORPHOMETRIC
APPROACH

2:00 p.m.
BROOKLYN MILLER (MacEwan University)
SPATIAL ANALYSIS OF PERMAFROST THAW ALONG
THE OLD CROW RIVER: EXPLORING CONTROLS
ON RETROGRESSIVE THAW SLUMP ACTIVITY AT A
REGIONAL SCALE

2:15 p.m.
PHOENIX ROWLEY (MacEwan University)
NUTRIENT-DRIVEN BIOEROSION IN THE DEVONIAN
REDWATER LEDUC FORMATION REEF

2:30 p.m.
RADHIKA SAINI (MacEwan University)
MAPPING EARLY DIAGENETIC ALTERATION IN
CARBONATE GRAINS FROM ABU DHABI USING
RAMAN SPECTROSCOPY

2:45 p.m.
TRISTAN SKRETTING (University of Lethbridge)
CHARACTERIZATION OF LONG-TOED SALAMANDER
MICROHABITAT STRUCTURE IN SOUTHWESTERN
ALBERTA PRIOR TO A MAJOR WILDFIRE

Oral Presentation Schedule

TUESDAY MAY 4 | **1:30 PM - 4:30 PM**

SESSION C3 | MEETING ID: 914 8300 1348

1:30 p.m.
KATRINA TAYLOR (University of Lethbridge)
ASSESSING MEDICAL ABORTION ACCESS IN
CANADA

1:45 p.m.
STEEL MCDONALD (University of Lethbridge)
SALIVARY METABOLOMIC BIOMARKERS INDICATIVE
OF STRESS VULNERABILITY AND RESILIENCE IN
SYRIAN REFUGEES

2:00 p.m.
PARKER MCNABB (University of Lethbridge)
HOW DOES BEING SICK IMPACT LEARNING IN A
SOCIAL SETTING?

2:15 p.m.
MALEEHA PANJWANI (University of Lethbridge)
REACH & GRASP: TWO SEPARATE MOVEMENTS OR
JUST ONE?

2:30 p.m.
BAILEY PORTER (University of Lethbridge)
INVESTIGATING THE DYNAMIC ACTIVITY OF
NEUROMODULATORS (NA, ACH, DA, 5-HT) DURING
CUE-BASED LINER TRACK EXPLORATION

2:45 p.m.
GISELLE TIEDE (University of Lethbridge)
THE METABOLOMIC PROFILE OF ALZHEIMER'S
DISEASE IN HIPPOCAMPAL BRAIN TISSUE

Oral Presentation Abstracts

STUDENTS HAVE 10 MINUTES TO PRESENT, FOLLOWED BY UP TO 5 MINUTES TO TAKE QUESTIONS

SESSION A1 | 3:30 PM - 6:30 PM

BIOL-03
CONSTRAINTS ON CYTOCHROME C OXIDASE I EVOLUTION IN FISH

Vanessa Boone | Supervisor: Matthew Morris
(Department of Biology, Ambrose University)

The mitochondrially encoded cytochrome c oxidase 1 (COI) gene in fish has the potential to provide information about constraints on protein evolution. COI is a subunit of complex IV, an enzyme in the electron transport chain which is made up of a series of electron transporters embedded in the inner mitochondrial membrane. The electron transport chain carries out functions essential to produce ATP. The COI gene was analyzed to investigate the mutations that take place in the mtDNA sequence in fish belonging to the orders of Argentiniformes, Clupeiformes, Cypriniformes, Esociformes, Osmeriformes, and Salmoniformes. The nucleotide and inferred amino acid sequences varied across the six orders as well as between species in the 37,976 sequences studied. Despite the observed variation, there were 119 nucleotide and 18 amino acid positions conserved across all the sequences. The degree of conservation was calculated for both the nucleotide and amino acid sequences to observe patterns in the sequence variation. Highly conserved regions may be informative in the evolution of the COI protein and the constraints on mutations in those regions.

BIOL-17
VARIATION OF THE COI GENE IN FISH

Cole Hartung | Supervisor: Matthew Morris
(Department of Biology, Ambrose University)

Given the widespread use of the mitochondrially encoded cytochrome c oxidase 1 (COI) gene in DNA barcoding, the readily available COI data allows for comparative analysis of the gene. Such analysis can give insight into evolutionary constraints on the protein. The COI protein is situated in the inner mitochondrial membrane, with components of the protein present in intermembrane, transmembrane and matrix regions. Functionally, COI is an enzyme which operates within the electron transport chain, responsible, in part, for ATP production in the cell. Variations of the COI gene across 10 orders of fishes was studied using 6378 mtDNA samples from the International Barcode of Life database. It was observed that nucleotides at 106 loci were invariant, while the other 1445 loci was observed to have differing amounts of variation. Variation of nucleotides in the first and second positions within a codon was observed to be significantly less than nucleotides in the third position of a codon. When the inferred amino acids were analyzed, 181 amino acids were observed to be invariant. Amino acid variance between intermembrane, transmembrane and matrix regions of the protein was found to be statistically different, with the most amino acid variation in the matrix region of the protein. This is the first part of a collaborative effort with Vanessa Boone.

BIOL-07

DETERMINING THE EFFECTS OF ANTIMICROBIAL PEPTIDE HUMAN B-DEFENSIN 2 ON STAPHYLOCOCCUS EPIDERMIDIS BIOFILM INHIBITION.

Fulnoor Cheema | Supervisor: Deborah Hemmerling
(Department of Biological and Environmental Sciences, Concordia University of Edmonton)

Bacterial resistance to antibiotics poses a challenge to the effective treatment of infectious diseases. Bacterial biofilms play a significant role in bacterial resistance to antibiotics. In order to combat resistance, the use of the antimicrobial peptide Human Beta Defensin 2 (HBD2) has been studied as a possible co-therapy with antibiotics. Staphylococcus epidermidis biofilm forming capacity plays a large role in its pathogenesis and antibiotic resistance. The purpose of this experiment was to determine if HBD2 would inhibit S. epidermidis biofilm formation. A biofilm formation assay was conducted by growing S. epidermidis biofilms in 96-well microtiter plates. Once this was achieved, biofilm inhibition assays were conducted by administering treatments to S. epidermidis of HBD2 at different concentrations, specifically 1uM and 0.5uM. The biofilm growth of treated wells was compared to growth of positive controls, which contained no defensin, and negative controls, which contained only media. Cell counts were conducted to determine the viability of cells. This was done to determine whether biofilm growth was being inhibited or if planktonic cells were being killed. The findings showed no significant difference between biofilm growth of the positive control and the 0.5uM treated wells. There was also no significant difference in biofilm growth between the positive control and the 1uM treated biofilms but also no significant difference between the 1uM treated biofilms and the negative control. The 1uM treated biofilms were inhibited enough that there was no significant difference between the negative control, however they were still prominent enough to show no significant difference between the positive control. There was no significant difference between cell counts for cells treated with HBD2 and control cells. In conclusion, it is possible HBD2 could inhibit S. epidermidis biofilm growth at higher concentrations, but further research is necessary.

BIOL-27

THE EFFECTS OF DIHYDROERGOTAMINE ON THE DEVELOPING CARDIOVASCULAR SYSTEM OF A CHICK EMBRYO

Alishia Pecorilli, Matthew Churchward (Co-Supervisor) Adriana Pecorilli (Assistant) | Supervisor: Mariola Janowicz
(Department of Biology, Concordia University of Edmonton)

Ergot alkaloids are a product of the parasitic fungus, ergot (Claviceps purpurea). Ingestion may produce life-threatening effects. Ergot poisoning can occur in either the gangrenous or convulsive forms. Since ergot inhabits forage and seed grains, livestock have an increased risk. Ergotamine, a prominent ergot alkaloid, is an agonist of the Serotonin 2B receptor subtypes (5-HT2BR), which are found in the cardiovascular system. Released 5-HT2BR is capable of eliciting vasoconstriction, valvulopathy, and prothrombotic effects. These findings have suggested that there may be impacts of ergotism on reproductive fitness or development of a gestating fetus, however prior research has not investigated this. I hypothesize that ergotamine will negatively impact heart and valve development in the chick embryo's cardiovascular system. I predict that higher concentrations of ergotamine will produce greater impacts. My prediction is supported by the known positive correlation of ergotamine and vasoconstriction of smooth muscles and heart valves. Three concentrations of dihydroergotamine were injected into embryos of 3 treatment groups (1µg/ml, 0.1 µg/ml, and 0.01µg/ml), at 1ml each. The control group did not receive dihydroergotamine. To assess heart and heart valves' development, the 24-96 hour slide mounted embryos were observed. Four of the day-14 embryos, from each treatment group, were used for heart dissections and analyses. The remaining four embryos were used for a Glycosaminoglycan-assay that tests for the presence of glycosaminoglycans, which are crucial for many functions of proper cellular growth. We have observed that as the concentration of dihydroergotamine increased the weights of the embryo's decreased. We predict that this trend in data will also be seen in overall heart development. If the data is consistent to what we have proposed this means, there will be a significant impact on animals that ingest ergot and, therefore, needs to be explored further.

BIOL-39

ASSESSING THE INHIBITORY EFFECT OF RETAPAMULIN ON ESCHERICHIA COLI (ATCC 13706)

Morgan Vercholuk, Carla Craveiro Salvado (Co-Supervisor) | Supervisor: Mariola Janowicz
(Department of Biology and Environmental Sciences, Concordia University of Edmonton)

Antimicrobial resistance (AMR) is a top 10 global threat to human health, as well as a major global health threat to animals and the environment. AMR can reduce the efficacy of antibiotic therapeutics, making treatment of bacterial infections difficult, expensive, and sometimes impossible. The increasing and wide-spread use of antibiotics has led to their global-scale misuse and abuse, resulting in the exponential emergence of antibiotic-resistant bacterial strains at alarming rates. The lack of speed in the development of new therapeutics for resistant bacteria is also a contributing factor to this global issue. Pleuromutilin, a diterpene natural product first isolated from the fungus Clitopilus passeckerianus, has been shown to be a potent inhibitor of Gram-positive (Staphylococcus aureus) and some Gram-negative bacteria (Haemophilus influenzae) by electively inhibiting bacterial translation. Retapamulin, the first drug in the new class of pleuromutilin antibiotics to be approved for human use as a topical antibiotic, was effective against Gram-positive bacteria, including methicillin-resistant Staphylococcus aureus (MRSA) in clinical trials. Although most strains of the Gram-negative bacteria Escherichia coli (E. coli) are harmless, several strains have developed antibiotic resistance. E. coli (ATCC 13706) is commonly found in wastewater, therefore susceptible to becoming antibiotic resistant. Given the observed inhibitory effects of retapamulin and pleuromutilin against Gram-positive bacteria and some Gram-negative bacteria, respectively, we hypothesize that retapamulin hinders the growth of E. coli (ATCC 13706). After performing the Kirby Bauer disk diffusion assay, we found that retapamulin inhibits E. coli at 500 ug/ml and it plateaus at 4000 ug/ml (ANOVA, df (9,20), F=121.3, p=1.8x10exp-15). We will also assess the minimum inhibitory and bactericidal concentrations. Thus far, our study suggests that E. coli ATCC 13706 is susceptible to retapamulin.

BIOL-36

PRAIRIE PLANT EXTRACTS THAT INCREASE THE LAG PHASE OF BACTERIAL GROWTH. A POTENTIAL SOLUTION FOR THE FOOD INDUSTRY TO REDUCE FOOD SPOILAGE.

Apsara Srinivas, Audrey Golsteyn | Supervisor: Sophie Kerneis
(Department of Biology, Lethbridge College)

Over the years, there has been an increased number of antibiotic-resistant bacteria. According to the WHO (World Health Organization), antibiotic resistance is one of the prime threats to global health and food security. One of the recommended measures of the WHO is to discover new antibiotics or to preserve the antibiotics that are on the market currently by finding alternative methods to fight or prevent infection. The Microbial Research laboratory at Lethbridge College is supporting these measures by testing the antibacterial properties of the plant species that are native to Alberta. Towards this goal, we have developed a unique plant extract library and are testing its effects upon several different parameters of bacteria biology. Bacterial growth can be divided into four distinct phases. The first phase, being the lag phase, is characterized by low metabolic activity and negligible cell division. The food industry in particular is interested in products that can increase the length of the lag phase of the bacteria as it prolongs the shelf life of their products. The Microbial Research laboratory has identified twenty plant extracts that significantly increase the duration of the lag phase of several bacteria including Staphylococcus aureus, Staphylococcus epidermidis and Citrobacter freundii. The plant extracts that decrease the length of the lag phase are from different plant families, which supports the hypothesis that there are different molecules involved in this effect. These phytochemicals could be a natural solution for industries looking for ways of reducing bacterial growth in their products.

BIOL-04

ISOLATION OF MICROSATELLITES FROM CYPRIPEDIUM PASSERINUM BY FIASCO

Noah Brooks | Supervisor: David McFadyen
(Department of Biological Sciences, MacEwan University)

With the current rate of biodiversity loss in plants, it is essential to develop and combine in situ and ex situ methods for an integrated approach to plant conservation. Central to integrated conservation approaches is the necessity for assessing genetic diversity within the threatened population. Among the tools available to assess genetic diversity is microsatellite analysis. Microsatellites are variable number tandem repeats, or short repetitive sequences within the DNA of an organism, that are useful due to their abundance within the genome, high mutation rate, and high levels of polymorphism. This project aimed to develop microsatellite markers for the vulnerable orchid, Cypripedium passerinum, for the purpose of assessing genetic diversity in populations within the Wagner Natural Area, Alberta, Canada. Fast Isolation by AFLP of Sequences Containing Repeats (FIASCO) was used to generate an (AC)n microsatellite enriched library from DNA samples of C. passerinum. A total of 83 clones from this library were isolated, 48 of which underwent sequence analysis to identify inherent microsatellite sequences. Approximately 56% of the isolated clones contained promising microsatellite sequences. Primers designed to amplify the identified microsatellite sequences will be useful tools in assessing the genetic diversity of C. passerinum populations, both inside and outside the Wagner Natural Area, and can potentially be applied to closely related species such as C. pubescens. Such genetic diversity assessment will inform conservation efforts of this threatened terrestrial orchid species.

BIOL-14

THE EFFECTS OF REPEATED MICRODOSING WITH LSD ON ZEBRAFISH (DANIO RERIO) BEHAVIOUR

Ethan Hagen, Melike Schalomon | Supervisor: Trevor Hamilton
(Department of Psychology, MacEwan University)

There has been a recent interest in the possible instrumental uses of LSD in humans. It is therefore important to further our understanding of its effects both acutely and when given repeatedly in animal models. Previous research using the zebrafish model has shown that lower doses (5-100 µg/l) had no effects on zebrafish behaviour when dosed in a single trial (acutely). However, it is unknown whether repeated dosing may have an impact. In this study a camera-based video tracking software system was used to record the movement of zebrafish after a repeated LSD exposure cycle. The dosing sessions lasted 30-minutes and they were at 0 (control), 1.5, 15, or 150 µg/l, daily for 10 days. On the 10th day of the cycle the fish were tested after dosing. The open- field and novel object approach tests were used as they are established anxiety-like behaviour and novelty paradigms, respectively. One week after the first round of testing we repeated the testing to examine potential withdrawal. We observed no significant effects on any aspect of behaviour after 10 days of dosing. There was a slight significant difference in anxiety-like behaviour during withdrawal testing. These results convey that there is likely little to no effects on anxiety and exploration after 10 days of microdosing in zebrafish, but there is possibility an effect during withdrawal.

BIOL-15

SCREENING PHYTOCHEMICAL EXTRACTS OF INVASIVE ALBERTAN WEEDS FOR ANTI-BIOFILM PROPERTIES

Jolie Hamel | Supervisor: Kimberley Harcombe
(Department of Biological Sciences, MacEwan University)

Biofilms, complex bacterial communities encased in a secreted matrix, are highly pervasive and problematic in health care settings. This lifestyle allows bacteria to anchor in a particular location and provides high intrinsic antibiotic resistance to the biofilm community, rendering biofilm infections difficult to remove once established. Effective anti-biofilm compounds for clinical use are lacking and are urgently needed. Plants may be an excellent natural source of anti-biofilm compounds given the prevalence of phytochemicals used as a defence mechanism. However, despite their rich phytochemical diversity, plants, and invasive weeds especially, have remained understudied for their anti-biofilm properties. In this study, we screened phytochemical extracts from invasive Albertan weeds for anti-biofilm properties against Escherichia coli, Bacillus licheniformis, Pseudomonas aeruginosa, and Staphylococcus aureus biofilms by testing the capability of the plant extracts to inhibit biofilm formation. Single-species adherent biofilms were grown in liquid culture in 96-well microtiter plates, and were exposed to increasing concentrations of a single plant extract during biofilm formation. To quantify total biofilm biomass, biofilms were stained with crystal violet and absorbance was measured at 595 nm. Preliminary analysis identified novel anti-biofilm activity in tested extracts, including an ethyl acetate extract from Leafy Spurge flowers and leaves. This work will contribute to existing knowledge of phytochemicals with anti-biofilm properties, which can be further developed into therapeutic treatments. In addition, this project provides preliminary identification of these compounds in invasive Albertan weeds, laying the groundwork for future studies on these extracts.

BIOL-28

THE EFFECTS OF VARYING CONCENTRATIONS OF HEMIN ON THE DIFFERENTIATION OF CHRONIC MYELOID LEUKEMIA (CML) CELL LINE K562

Hailey Pon | Supervisor: Nina Bernstein
(Department of Biological Sciences, MacEwan University)

Chronic myeloid leukemia (CML) results from a chromosomal abnormality that leads to uncontrolled division of red blood cell precursors. Typically, these cells undergo erythrocytic differentiation during the production of new blood cells. However, due to uncontrolled cell division, these immature and non-functional cells are unable to undergo differentiation and, as a result, build up in the bone marrow. Hemin, a compound derived from blood, has been shown to induce differentiation in CML cells stopping their uncontrolled division by making these cells mortal. This study aimed to further characterize hemin and determine the optimal concentration that can induce differentiation in a CML cell line, K562, as evidenced by an increase in the expression of the molecular marker gamma-globin. To identify the optimal hemin concentration, the rate of proliferation and the level of gamma-globin expression were monitored in response to hemin concentrations of 20 uM, 40 uM, 60 uM, and 80 uM with DMSO or dilute NaOH as the solvents. We performed a growth curve analysis and assessed the level of hemoglobin expression using benzidine staining. A clear trend was observed for hemin in DMSO, showing that concentrations of 40 uM and higher decreased cell proliferation and viability. In addition, an increase in benzidine staining was seen between DMSO and 20 uM hemin, indicating elevated levels of hemoglobin expression. To verify that the observed increase in hemoglobin level corresponds to increased expression of gamma-globin, western blotting was used. These findings will help characterize differentiation therapy as an alternative treatment for CML, in which cells are induced to undergo differentiation and then controlled cell death. This development is important since current treatments (Imatinib and related compounds) are susceptible to loss of efficacy due to the development of drug resistance.

SESSION A2 | 3:30 PM - 6:30 PM

BIOL-33

WHAT CAN NORTHERN PIKE (ESOX LUCIUS) STOMACH CONTENTS REVEAL ABOUT POST-MANAGEMENT COMMUNITY DYNAMICS IN LAC LA BICHE, ALBERTA?

Jennifer Roth | Supervisors: David Locky, Mrinal Das
(Department of Biological Sciences, MacEwan University)

Altering top predator density within freshwater lakes is often done to restore commercially important species; however, such management may inadvertently result in trophic cascades or dietary shifts in existing predator populations. The 2005 Fisheries Restoration Program in Lac La Biche, Alberta, was established to recover walleye (Sander vitreus) populations through a combination of double-crested cormorant (Phalacrocorax auritus) culls and intensive stocking. Although walleye abundance increased dramatically, other dominant piscivores' response to management actions, namely the Northern pike (Esox lucius), is less clear. Pike dietary shifts in response to stressors are extremely community-dependent due to their opportunistic feeding strategy. Pike may incorporate more invertebrates into their diets when interspecific competition for prey fish is high; however, the importance of invertivory remains understudied. A stomach content analysis was performed on 121 pike stomachs sampled during Fall Walleye Index Netting Surveys from 2009 to 2013 to elucidate how northern pikes' dietary composition and feeding strategies have changed in response to management actions in Lac La Biche. Preliminary trends suggest that piscivory was the most common feeding style, with yellow perch the dominant prey species. However, the diversity of fish prey species decreased over time. Invertivory and mixed feeding habits were less common, particularly between 2010-2013, yet showcase the pike's opportunistic feeding habits. There was also a high proportion of empty stomachs, with an average of 45% (±0.07 SE), reflecting strong asynchronous feeding. The proportion of empty stomachs roughly doubled between 2009 and 2010-2013, whereas the other feeding types decrease correspondingly. Further analysis will clarify the role predator biomanipulations have on community dynamics and increase our knowledge of pike dietary composition and the relative importance of invertivory.

BIOL-35

INVESTIGATION OF 30 DAYS OF EXPOSURE TO OIL SANDS PROCESS-AFFECTED WATER IN ZEBRAFISH (DANIO RERIO)

Shivani Solanki, Nathan Nadolski, Courtney Bailey, Erica Ingraham, Matthew Ross, and Warren Burggren
Supervisor: Trevor J. Hamilton
(Department of Psychology, MacEwan University)

Oil sands process-affected water (OSPW) is the by-product of bitumen extraction from the oil sands industry in northern Alberta, Canada. OSPW exposure can cause reproductive and behavioural changes in native and non-native fish species. In our study, we used zebrafish (Danio rerio), which are sensitive to both anxiolytic and anxiogenic substances and have already been used as a model species for effects of OSPW exposure. We administered diluted OSPW (10% OSPW in dechlorinated tap water) for 30 days. Fish were observed at day 10, 20, and 30 of OSPW exposure and at day 25 and day 60 after return to control water. Control groups underwent identical procedures without OSPW. A motion-tracking software system was used to monitor the behaviour of groups (shoals) of five fish in fifteen-minute trials. The average velocity, interindividual distance (IID) between shoalmates, and time in various arena zones were quantified. Velocity of OSPW-exposed fish decreased significantly (24%) from day 10 to day 30 and increased significantly (28%) from day 30 to recovery day 60. By day 10, OSPW-exposed fish were spending significantly more time in the center of the arena than control fish. Fish spent more time in the thigmotaxis zone (outer edge) during day 20 and 30 of OSPW exposure than during the recovery period. Our results suggest that exposure to OSPW can have varied, but possibly reversible, effects on zebrafish behaviour.

BIOL-37

ANTIMICROBIAL ACTIVITY OF PHYTOCHEMICALS EXTRACTED FROM ALBERTAN INVASIVE WEEDS

Brittany Supina | Supervisor: Kimberley Harcombe
(Department of Biological Science, MacEwan University)

Due to the incessant rise of antibiotic-resistant bacteria, new antimicrobial agents are required for controlling infections. Phytochemicals are secondary metabolites produced by plants that are released into the environment to defend them against pathogens and pests. These phytochemicals are structurally and functionally diverse, making them a potential source of new antimicrobial compounds to combat resistant bacteria. Most phytochemical studies have focused on medicinal and edible plants, leaving invasive species largely understudied. However, invasive weeds offer a promising source of new antimicrobial compounds because they can upregulate and diversify their phytochemical production during the invasion of new habitats. In this research, we explored the antimicrobial activity of Albertan invasive weed species collected in the Edmonton area. Using successive Soxhlet extractions with hexane, ethyl acetate, and methanol, we extracted different classes of phytochemicals from 11 invasive plant species. These extracts were tested for their ability to inhibit the growth of a range of bacterial types using Kirby-Bauer disk diffusion assays. Preliminary characterizations of extracts against Escherichia coli, Bacillus subtilis, Pseudomonas aeruginosa, and Staphylococcus aureus identified inhibitory activity for multiple plant species including woolly burdock (Arctium tomentosum) and common tansy (Tanacetum vulgare). These findings provide insight into the antimicrobial potential of Albertan invasive weeds and serve as a basis for future chemical and bioactivity characterizations of these plant species.

BIOL-41

HUMAN CHRONIC MYELOGENOUS LEUKEMIA K562 CELLS UNDERGO ERYTHROCYTIC DIFFERENTIATION AND CELL CYCLE INTERRUPTION IN RESPONSE TO PMEA (9-(2-PHOSPHONYL-METHOXYETHYL)-ADENINE)

Brittany Wiseman | Supervisors: Kim Harcombe, Nina/Bernstein
(Department of Biological Sciences, MacEwan University)

When hematopoietic stem cells undergo disruption of cellular differentiation during hematopoiesis, it can result in the formation of cancer cells. Differentiation therapies are being investigated as a new type of cancer treatment that involves the induction of cancer cells to undergo cellular differentiation into homologues of normally functioning cells, such as erythrocytes, which can then undergo cell death at an accelerated rate compared to cancer cells. In this particular study, the ability of human chronic myelogenous leukemia (CML) K562 cells to undergo erythrocytic differentiation in response to the inducing agent PMEA (9-(2-Phosphonyl-methoxy ethyl)-adenine) is investigated. PMEA has been shown to both halt cell replication by stalling S-phase, and promote erythrocytic differentiation in K562 cells. In order to further test the effectiveness of this inducer to promote erythrocytic differentiation, the concentration of gamma-globin (a protein subunit of fetal hemoglobin) was measured in both induced and uninduced K562 cell cultures via qRT-PCR and western blotting. The ability of PMEA to halt cell cycle progression was also measured via a cell growth curve and the presence of hemoglobin was measured via benzidine staining. The results indicate that those cells exposed to PMEA underwent slowed cell replication and expressed hemoglobin, and subsequently gamma-globin, at a higher concentration than those cells not exposed to PMEA. In summary, the findings reveal that PMEA was able to promote the erythrocytic differentiation of K562 cells, and provide information that supports differentiation therapies as a method for cancer treatment in the future.

BIOL-42

IDENTIFYING THE NUCLEAR LOCALIZATION SIGNAL OF THE ARABIDOPSIS

TRANSCRIPTION FACTOR FLOWERING LOCUS C

Brittany Wiseman | Supervisor: Melissa Hills
(Department of Biological Sciences, MacEwan University)

The goal of this undergraduate honours research project is to design a research strategy to identify the Nuclear Localization Signal (NLS) of the Arabidopsis thaliana MADs box transcription factor Flowering Locus C (FLC), and to begin the cloning and plant transformation of key controls required for this objective. Nuclear localization of proteins requires a specific amino acid sequence, called the Nuclear Localization Signal (NLS). The NLS of FLC has not yet been characterized, though previous work on Arabidopsis has established conserved structural-functional domains within FLC. The NLS within other MADs box proteins varies in its specific sequence, but is generally located within the MADs box domain around the N-terminal region of the polypeptide, which is a conserved region amongst MADs box proteins. I have created an FLC gene construct to be used with the GreenGate cloning system which will ultimately serve as a positive control showing nuclear localization in planta. I have also established the components necessary for the creation of a negative control line of Arabidopsis expressing GFP alone, which is not expected to nuclearly localize. Finally, I have completed a literature review to explore the existing understanding of NLS structure in general, in MADs box transcription factor proteins, and in other plant transcription factors, to propose mutations that might disrupt the NLS sequence within FLC. This work aims to fill a knowledge gap in regards to the mechanism of nuclear localization of FLC and will ultimately contribute to our understanding of nuclear localization in general.

BIOL-01
EVALUATION OF MYOD GENE EXPRESSION IN C2C12 CELLS CULTURED ON EXTRACELLULAR MATRIX PROTEINS

Rashida Aamir | Supervisor: Laura Atkinson
(Department of Biology, Mount Royal University)

The murine myoblast cell line, C2C12, is frequently used to study skeletal muscle formation during myogenesis of myoblasts proliferation and differentiation into multinucleated myotubes on standard dishes. However, these dishes lack cells' interactions with extracellular matrix (ECM) rich microenvironment that is required for the complicated process of skeletal muscle formation in vivo. Studies show that ECM proteins, fibronectin and collagen coating, promote adhesion and proliferation of myoblasts in vitro as well as they could impact gene expression of muscle regulatory factors (MRFs), involved in skeletal muscle cells' formation in vitro which needs to be examined. Here, this study aims to investigate the effect of the ECM coated proteins, fibronectin and gelatin, on C2C12 differentiation by studying mRNA expression of a transcription factor, MyoD, which is also a master regulator in myogenic differentiation, throughout myogenesis as compared to those without the coating. Phase-contrast microscopy was used to confirm and analyze relative morphological changes at myoblast, days 0, 4, and 7. Reverse transcriptase reaction converting extracted RNA into complementary DNA (cDNA), real-time quantitative PCR (qPCR) was performed. In subsequent analysis, the Pfaffl method was used to calculate relative gene expression after normalizing the data with GAPDH. This study has the potential to contribute to the understanding of the processes involved in myogenesis and thus could help in finding a treatment for dysfunctional skeletal muscle due to injury, muscle diseases, and ageing, in the future.

BIOL-23

MYOGENIC DIFFERENTIATION INDUCED BY CELL-TO-CELL CONTACT VERSUS SERUM STARVATION: EFFECTS ON MYOD, MYOGENIN, AND MYOSIN HEAVY CHAIN MRNA EXPRESSION IN C2C12 CELLS

Daniel Major, Emma Bogner, Charleigha Cao-Gagnon, Jessica Lee, Jaiden Peeace, Lindsay Leahul, Ava Zare
Supervisor: Laura Atkinson
(Department of Biology, Mount Royal University)

C2C12 murine myoblasts are commonly used in cell culture to study myogenesis - a process in which myoblasts differentiate and fuse to form mature myotubes. Regulatory factors MyoD and myogenin (MyoG) in addition to proteins involved in the contractile apparatus (such as myosin heavy chain IIb (MyHCIIb)) are good markers of myogenic progression. Differentiation of C2C12 myoblasts may be induced by serum starvation or direct cell-to-cell contact. Currently, serum starvation is used in the majority of studies exploring in vitro myogenesis; however, the methods vary considerably and the impact of this intervention on gene expression is unclear. This study provided preliminary evidence for how varying serum conditions may impact the mRNA expression of MyoD, MyoG, and MyHCIIb during myogenesis. C2C12 cells were supplemented with 10% fetal bovine serum (FBS) and differentiated by serum starvation in 2% horse serum when the cells reached 100% confluency (day 0) or by cell-to-cell contact with serum remaining at 10% FBS. Samples were collected at the myoblast stage (~60 - 90% confluency), and days 0, 1, 5, 7 and 12 of differentiation. The mRNA expressions of each target gene relative to the reference gene GAPDH were assessed over the course of myogenesis using reverse transcription and qPCR. Cell morphology was monitored using phase contrast microscopy. This research provides important information about how culture conditions may impact differentiation and could inform future experiments investigating protein expression levels and optimization of muscle cell growth for applications including tissue bioengineering and alternative meat production.

BIOL-32

EFFECT OF GROWTH AND DIFFERENTIATION MEDIA ON MRNA EXPRESSION LEVELS OF M-CADHERIN AND MYOGENIN DURING MYOGENESIS OF C2C12 MYOBLAST CELLS

Laura Reyes Palacios, Meron Feleke, Diana Carolina Ortiz Pérez, Noha Zeineldin | Supervisor: Laura Atkinson
(Department of Biology, Mount Royal University)

The C2C12 cell line is used to study myogenesis as it can proliferate at the myoblast stage and will withdraw from the cell cycle, entering differentiation when certain conditions are met. These events can be followed through gene expression of differentiation markers like m-cadherin and myogenin, which are known to have specific roles in the fusion and differentiation of myoblasts. It is unclear if serum conditions impact the mRNA expression levels of essential proteins in C2C12 cells. According to the ATCC protocol, C2C12 cells proliferate and differentiate in 10% fetal bovine serum (FBS). However, many previous studies have used 2% horse serum (HS) to induce differentiation. This study investigates the impact of 10% FBS vs 2% HS differentiation media on m-cadherin and myogenin mRNA expression of C2C12 cells in myogenesis. We hypothesized that HS media would produce a higher rate of differentiation and mRNA expression of the two target proteins in comparison to FBS. To achieve this, C2C12 myoblast cells were collected at the myoblast stage and days 0,4,7, and 11 of differentiation. Phase-contrast microscopy was used to confirm the stages chosen for analysis. RNA was extracted from the cells and validated for purity and quality. Finally, RNA was reverse transcribed for cDNA synthesis and designed primers were used to perform quantitative RT-qPCR to measure m-cadherin and myogenin mRNA expression levels. Understanding whether culture conditions impact C2C12 myogenesis may allow in vitro studies to more accurately represent myogenesis in vivo.

BIOL-34

EXPRESSION OF RISK GENES LINKED TO VITAMIN D RECEPTOR SUPER ENHANCER REGIONS AND THEIR ASSOCIATION WITH PHENOTYPE SEVERITY IN MULTIPLE SCLEROSIS: PILOT STUDY

Amarpreet Sangha, Mehul Gupta, Matthew Joel, Kristina Martens, Luanne M. Metz, AP J. de Koning, Gerald Pfeffer
Supervisor: Sarah Orton
(Department of Biology, Mount Royal University)

Unravelling gene-environment interactions in multiple sclerosis (MS) is challenging, and vitamin D receptor super enhancers (VDSEs) may modulate genetic risk variant and environment-based vitamin D interactions. Previous studies have shown that VDSE regions are enriched in MS risk variants. mRNA expression in total of 64 patients with contrasting MS severity was quantified in select genes. First, RNA-seq was performed on a discovery cohort (n=10 mild phenotype; n=10 severe phenotype patients) and six genes previously shown to be associated with MS risk SNPs in VDSE regions were analyzed. mRNA from four genes showing a positive association (GRINA, PARP10, LRG1, and PLEC) were then quantified using digital droplet PCR (ddPCR) in a validation cohort (n=33 mild phenotype; n=11 severe phenotype patients). Of the four MS-VDSE genes showing a significant association in the validation cohort, three showed a significant difference in expression between the mild and severe phenotypes: GRINA ($p = 0.0138$), LRG ($p = 0.0157$), and PLEC ($p = 0.0391$). These genes were upregulated in the severe phenotype. Genes associated with MS risk variants in VDSE regions were shown to have differential expression based on disease severity ($p < 0.05$). The current findings should be expanded to further VDSE-MS candidates to better understand the significance of VDSEs in modulating gene-vitamin D interactions in MS.

BIOL-26

SURVEY FOR MACROBIOTUS OCCIDENTALIS AND DIAFOROBIOTUS SPP. IN VICTORIA, BRITISH COLUMBIA, CANADA, AND FIRST IDENTIFICATION OF PARASCON SP. IN CANADA

Kiara O'Shea, | Supervisor: Gary Grothman
(Department of Biology, St. Mary's University)

Changes in morphological descriptions create challenges in tardigrade identification and classification. Utilizing the description by Murray (1910) for Macrobiotus occidentalis, this study surveyed the tardigrade fauna in Victoria, British Columbia, Canada in an attempt to locate M. occidentalis, or similar tardigrades from the genus Diaforobiotus. M. occidentalis was first identified by Murray (1910) in this location, but none of the original specimens were preserved. All specimens in the present study were permanently mounted on standard microscope slides using polyvinyl alcohol to allow the observation of the sclerified morphological features during the taxonomic classification process. While neither M. occidentalis nor Diaforobiotus spp. were found during this study, a Parascon sp. was successfully identified. This Parascon sp. is the first member of this genus to be recorded in Canada. The genus Parascon includes two species, P. schusteri and P. nichollsae, but the observed specimen could not be successfully classified as either species. Throughout this study, challenges in identifying M. occidentalis occurred, as the morphological description has been continually modified from the original description by Murray (1910). These modifications, discussed in detail, highlight a potential species complex and the need for re-examination of the morphological description of M. occidentalis.

CHEM-06

SYNTHESIS AND EVALUATION OF ENVIRONMENTALLY FRIENDLY WOUND-CARE PRODUCTS--APPLICATION OF GREEN CHEMISTRY IN UNDERGRADUATE RESEARCH

Jared VanderZwaag, Hechao Du | Supervisor: Liza Abraham
(Department of Biology, Ambrose University)

This project focuses on the development of two bioinspired, environmentally-friendly wound-care products derived from chitosan and two naturally occurring aldehydes, citronellal and cinnamaldehyde. The two Schiff base products were characterized using FTIR and SEM and evaluated for antimicrobial properties. Results suggest that both Schiff base products are highly bioactive and could indeed have value in wound-care. The current paper is an example that highlights the application of green chemistry toward valuable undergraduate research and the ability of institutions to offer undergraduate research opportunities with limited funding and infrastructure.

CHEM-01

QUANTIFICATION OF FRUCTOSE AND GLUCOSE BY HPLC-UV AND OZASONE DERIVATIZATION

Ramanjot Kaur | Supervisor: Patrick Kamau
(Department of Math and Physical Sciences, Concordia University of Edmonton)

Honey consists of majority of carbohydrates, in particular fructose and glucose, and minor components like water, vitamins, pollen and other substances. The amount of carbohydrates present in honey depends on the source of nectar, type of plants and the environmental conditions. The amount of fructose and glucose can be as high as about 70 – 80 % of total composition. Fructose has a lower glycemic index compared to glucose which potentially could have a significant effect on people with diabetes. In addition, consumption of products with high levels of fructose and glucose can lead to weight gain. Different types of honey have different amounts of glucose and fructose present. However, on the list of ingredients in honey only the total amount of sugar is given but not the individual amounts of fructose and glucose. So, in this research project individual concentrations of glucose and fructose in various honey samples will be analyzed using reverse phase HPLC (High Performance Liquid Chromatography) and the formation of osazone derivatives. UV-HPLC was used to separate glucose and fructose, which co-elute, from other components that also absorb at the 195 nm detection wavelength. Osazones were formed to find the mass of total glucose and fructose in five honey samples by derivatization with phenylhydraine hydrochloride which caused the sugars to selectively precipitate. Osazones of glucose and fructose have different times of precipitation, fructose crystals form at about 2 minutes and Glucose at about 5 minutes. Using the total mass and absorption data from HPLC analysis, the amounts of fructose and glucose will be determined mathematically. Fructose and glucose masses obtained from the osazone method will be used to compare the masses determined from HPLC-UV.

CHEM-02

SYNTHESIS OF HEPTA-1,3,6-TRIEN-5-OLS FOR POTENTIAL 8PI ELECTROCYCLIZATIONS

Bryce Kirk | Supervisor: Owen Scadeng
(Department of Math and Physical Sciences, Concordia University of Edmonton)

Hepta-1,3,6-trien-5-ols have the potential to act as electrocyclization precursors in anionic 7 carbon/8pi conrotatory transformations. A concise synthesis of these trienol substrates is discussed. The sequence of Vilsmeier Haack type

reaction, 1,2-vinyl addition, and a Suzuki-Miyaura cross-coupling allows for multiple points of elaboration and alkenyl stereocontrol. Finally, the alcohol can be converted to groups such as silyl ethers or carbamates to probe the impact on carbolithiation.

CHEM-05

ANALYTICAL METHOD DEVELOPMENT FOR HPLC QUANTITATION OF IBUPROFEN IN THREE PHARMACEUTICAL PRODUCTS

Mandeep Singh | Supervisor: Makan Golizeh
(Department of Mathematical and Physical Sciences, Concordia University of Edmonton)

Introduction: Ibuprofen is present in different types of medicine such as Advil, Motrin and Nuprin. It belongs to nonsteroidal anti-inflammatory drugs (NSAID). NSAID is a drug class that is used for various purposes such as pain management, decreasing fever and reduction of inflammation. The NSAID has several side effects such as gastrointestinal ulcers, heart attack and kidney diseases. To determine the percentage of ibuprofen in selected products, including Advil, Motrin and Nuprin, we will use high-performance liquid chromatography (HPLC). HPLC is a powerful technique used in analytical chemistry to identify, determine and quantify the components of an unknown sample. HPLC is used in many fields, such as pharmaceutical and medical research and it has the ability to produce extremely high-quality results.

Method: Three pharmaceutical products containing ibuprofen were obtained and the quantity of ibuprofen in those samples was determined. Two HPLC methods were developed for quantitation of ibuprofen in tablets using standard addition or external calibration. Method parameters such as sample preparation, type of column, and elution parameters were optimized. The accuracy and reproducibility of these methods were compared. In standard addition, the standard was directly added to unknown to minimize matrix effect. For external calibration, data from a standard curve was used to quantify HPLC peak area to analyte concentration.

Expected Results: I will determine the amount of ibuprofen present in different samples (tablets) using an accurate and reproducible HPLC method coupled with standard addition or external calibration.

CHEM-07

THE IMPACT OF PRO OXIDANT BIOMETALS ON NON-ENZYMATIC GLYCATION UNDER PHYSIOLOGICAL CONDITIONS

Thérèse Wilson-Rawlins | Supervisor: Makan Golizeh
(Department of Mathematical and Physical Sciences, Concordia University of Edmonton)

Introduction: The Maillard Reaction, known as the 'browning reaction' gives rise to potentially toxic compounds and reduces the nutritional value of foods by degrading essential amino acids such as lysine and arginine. This is the cause of the savoury smell and flavour of our foods. This reaction is also considered to be a 'non-enzymatic' reaction dubbed glycation. Glycation is the covalent attachment of a reducing sugar to a protein or a lipid. The Maillard reaction generally only begins to occur above 140 degrees Celsius. Advanced glycation end-products AGEs are cytotoxic, products that have dastardly effects on metabolic health. AGE formation can be catalyzed by prooxidant biometals copper, zinc, iron and manganese. AGE levels have been used as a biomarker in diseases such as diabetes and glaucoma as well as indicators of protein damage. The focal point of this research was to simulate glycoxidative stress (GOS) conditions in vitro and assess the role of the abundant biometals Fe and Cu in GOS and glycation using microwave radiation to expedite the process.

Method: The ideal reaction conditions for the biosynthesis of the AGE carboxymethyllysine (CML)/ Maillard Reaction Product (MRP) using glucose and lysine under microwave radiation and conventional/physiological conditions was optimized. UV-Vis and TLC were used to assess the impact of reaction environment such as pH, biometal and

microwave efficiency on MRP formation. GC-MS will be used to detect and quantitate MRPs after biosynthesis.

Preliminary Results: UV-Vis data indicates that iron is a more effective catalyst for the formation of MRPs than copper as all of the MRPs had a greater absorbance, indicating a greater degree of browning. A pH of 7.4 is the ideal environment for MRP formation. MRP formation is expedited using microwave radiation. MRPs are detected even after just 1 minute of microwave treatment. Biometals directly affect the reaction kinetics while pH affects the type of MRP formed.

CHEM-04
CHROMATOGRAPHIC AND NMR ANALYSIS OF ALBERTAN INVASIVE WEED SPECIES

Radhika Saini | Supervisor: Tina Bott
(Department of Physical Sciences, MacEwan University)

Antimicrobial resistance has rapidly increased since the first discovery of antimicrobial agents, however, the development of antimicrobial agents has lagged significantly behind. Our group's previous study determined the preliminary antimicrobial activity of six Albertan invasive weed species against the bacterial species E. coli, P. aeruginosa, S. aureus, and B. subtilis. To further investigate these observations, each of these weed extracts' chemical components needed to be examined in more detail. The overall fractioning and biological testing process will continue to identify active phytochemicals that the antimicrobial activity can be specifically assigned to. This study's primary objective was to use chromatography to fractionate the crude extracts of interest and identify some of the extracts' phytochemicals. Several crude extracts of Euphorbia esula (leafy spurge flower and leaf, root and stem) and Linaria vulgaris (yellow toadflax) were analyzed by thin-layer chromatography and fractionated using column chromatography. Phytochemical characterization was subsequently performed using nuclear magnetic resonance (NMR) spectroscopy and mass spectrometry. Each crude extract was divided into four to nine fractions, and further results of this study will be presented.

CHEM-03
QUANTUM MECHANICAL TREATMENT OF POST-TRANSCRIPTIONALLY MODIFIED URACIL BASE PAIRS

Bhadra Pandya, Kohl Yee, Preethi Seelam Prabhakar | Supervisor: Stacey Wetmore
(Department of Chemistry and Biochemistry, University of Lethbridge)

The canonical nucleobases in transfer RNA (tRNA) regularly undergo post-transcriptional modifications. To date, over 100 post-transcriptional modifications have been identified, many of which are conserved throughout the three domains of life (Eukarya, Bacteria, and Archaea). As a result, the functionally-relevant implications of these modifications are significant enough to warrant the thorough analysis of their impact on tRNA structure and function, and more broadly, protein translation. In particular, modifications to the base at the 34th position (wobble position) have been proposed to be instrumental in fine-tuning base-pair interactions in the codon– anticodon complex. Certain modifications to the base occupying the wobble position may enhance the decoding capacity of tRNA species, increase translational fidelity, and/or strengthen codon–anticodon interactions in the anticodon stem-loop region (ASL). These potential functions underscore the importance of studying the changes these conformations confer in the context of base-pair interactions. Since modified uracil nucleobases have garnered much interest in recent years due to their ubiquity and functional importance as it relates to various cellular processes, the present work studies the impact of 13 different modifications on the base-pairing properties of uracil with respect to the wobble position in tRNA. Specifically, quantum mechanical (QM) calculations were performed in order to elucidate the characteristics of modified uracil base pairs, both with canonical and non-canonical pairing partners. Insights into the base-pair geometry and thermodynamic properties provided by QM methodology help us understand the overall integrity of the interactions between nucleobases and the potential impact of the modifications on the function of tRNA.

HS-03

DO INCREMENTAL THEORIES OF WELL-BEING AND OTHER WELL-BEING BELIEFS PREDICT PROSOCIAL SPENDING?

Carley Aquin | Supervisor: Andrew Howell
(Department of Psychology, MacEwan University)

Research has revealed that prosocial spending is associated with greater well-being than is personal spending. Given this link, well-being beliefs may predict the degree to which people endorse prosocial spending relative to personal spending. In Study 1, it was predicted that incremental mindsets toward well-being and eudaimonic well-being beliefs would be associated with prosocial spending and autonomous reasons for prosocial spending. Results showed that undergraduate students (N = 288) with greater eudaimonic and lower hedonic well-being beliefs demonstrated an increased preference for prosocial spending and autonomous reasons for prosocial spending, controlling for socially desirable responding. The implications of the current research will be discussed, including mechanisms by which well-being beliefs are or are not associated with prosocial spending.

OTHER-02

EMPATHY, SELF-AWARENESS AND PET-OWNERSHIP

Miray Helmy | Supervisor: Eric Legge
(Department of Psychology Department, MacEwan University)

Empathy is defined as the ability to share feelings and emotions of another individual (Daly & Morton, 2009). A person's level of empathy can be affected by many factors, such as exposure to childhood trauma (Greenberg et al., 2018), mindfulness training (Birnie et al., 2010), and childhood pet ownership (Daly & Morton, 2006; Vidović et al., 1999). It is the last of these items that is of interest to the present study. Specifically, it is unclear whether one's change in empathy is due to pet ownership itself, or the result of changes in other personal factors that tend to coincide with pet ownership. The present study is therefore designed to expand on our understanding of why pet ownership is associated with empathy change, and will assess the relationship between empathy and one's relationship with animals, the bond an individual has with their pet, and or one's level of self-awareness (the ability to distinguish oneself and one's values from others, Froming et al., 1998), among others. Therefore, we predict that in general, owning a pet will be associated with higher levels of human-centered and animal-centered empathy. However, we also predict that the strength of the pet-owner bond, and personal factors such as one's level of self-awareness, will be critical modulating factors for the relationship between pet-ownership and empathy. Specifically, we predict that individuals with a stronger bond with their animal, and higher levels of self-awareness, will have higher empathy scores than those who have weaker bonds with their animals, or lower levels of self-awareness.

OTHER-10

USING TAGTEACH TO INCREASE CREATIVE PLAY BEHAVIOR IN CHILDREN WITH AUTISM

Jade Radke | Supervisor: Miranda Macauley
(Department of Psychology, MacEwan University)

Play is an everyday activity during childhood and is thought to be essential for development (Brodin, 1999). Nevertheless, many children with autism tend to engage in rigid play behavior, often only playing with the same toys in the same way or not playing flexibly enough to include other children or parents in their playtime (Kasari et al., 2011). This rigidity may, in turn, impede their ability to form social relationships with their peers and hinder the development

of communication skills. Accordingly, increasing creative play behavior in children with autism may decrease rigid and solitary play and increase communication skills and social relationships. One method that may be useful for improving this skill is Teaching with Acoustical Guidance (TAGteach). This intervention involves shaping behavior through positive reinforcement using an auditory stimulus (Persicke et al., 2013). Given the behavioral principles that underlie its methodology, we predicted that TAGteach would be useful for increasing creative play behavior in two children with autism. A multiple baseline across participants design was used. Because of the COVID-19 pandemic, the study was run via encrypted real-time video conferencing. Social validity of the intervention was assessed at the end of the study. Overall, we found a slight increase in creative play behavior across sessions for both participants. Additionally, the individuals who implemented the TAGteach intervention rated the intervention moderately to extremely positive on a post-test social validity measure. These findings offer initial insight into the use of TAGteach via telehealth for children with autism.

HS-06

THE SIGNIFICANCE OF HIGH ALTITUDE ACCLIMATIZATION ON THE HYPEROXIC VENTILATORY WITHDRAWAL TEST PERFORMED ON NATIVE LOWLANDERS

Godi Jibi | Supervisor: Trevor Day
(Department of Health Sciences, Mount Royal University)

The transient hypoxic ventilatory response is the most common assessment of ventilatory acclimatization during high altitude ascent, as peripheral chemoreceptors become increasingly sensitized in response to chronic hypoxia. In contrast, the transient hyperoxic withdrawal (HVW) test uses portable O2 available on expeditions, and may better assess ventilatory acclimatization of chronically hypoxic participants. We hypothesized that the HVW would be larger following 7-days of ascent to 4240 m than a low altitude acute hypoxic control group, thus having utility in detecting ventilatory acclimatization during ascent. Using separate recruitments, we tested two groups in different contexts. In Part A, the HVW of 14 participants were assessed during acute, steady-state hypoxia (~30-min; FIO2 13.5-14%) at 1045 m (PATM ~665 mmHg). In Part B, 12 participants were observed for 7 days of incremental ascent to 4240 m (PATM ~460 mmHg), while taking prophylactic acetazolamide. While breathing roughly equivalent PIO2 of ~85 mmHg at baseline, both groups inhaled single tidal breaths of 100% O2. The HVW was quantified as the change in inspired ventilation from baseline to the smallest breath following hyperoxic stimulus, indexed to the change in oxygen saturation (SpO2;%) from baseline to peak, following the hyperoxic breath (i.e., ventilatory response/oxygen stimulus). We found that the HVW values from acute and acclimatized hypoxic participants had a mean of 0.34±0.23 and 0.53±0.24 L/min/% (P=0.03), respectively. Our results suggest that the transient HVW test adequately detects peripheral chemoreceptor sensitization and ventilatory acclimatization during altitude ascent.

HS-10

CEREBROVASCULAR RESPONSES DURING VOLUNTARY BREATH HOLDING ARE LARGER THAN REBREATHING

Anthony Marullo, Christina Bruce, Jamie Pfoh, Uday Chauhan, Maria Abrosimova, Emily Vanden Berg, Rachel Skow, Margie Davenport, Nicholas Strzalkowski, Craig Steinback | Supervisor: Trevor Day
(Department of Biology, Mount Royal University)

Both voluntary breath-holding (BH) and rebreathing (RB) of expired air elicit changes in respiratory gas (CO2 and O2) chemostimuli at the metabolic rate. These chemostimuli elicit synergistic increases in cerebral blood flow (CBF), and sympathetic nervous system activation, increasing systemic blood pressure. The extent that superimposed changes in blood gases and increases in blood pressure affect the CBF responses during BH vs. RB is unclear. We previously recruited 23 healthy participants and instrumented them with a finometer (beat-by-beat mean arterial blood pressure; MAP), transcranial Doppler ultrasound (middle and posterior cerebral artery velocity; MCAv, PCAv) and a mouthpiece with sample line attached to a dual gas analyzer to assess the pressure of end-tidal (PET)CO2 and O2. Participants carried out two protocols in randomized order: a maximal, voluntary end-inspiratory BH and RB test. A breath-by-

breath stimulus index (SI) was calculated as PETCO2/PETO2 during RB, whereas the end-tidal gas values used to calculate SI were interpolated during BH from initial and break point values. Cerebrovascular reactivity (CVR) was calculated as the MCAv or PCAv/SI, and MAP reactivity (MAPR) was calculated as the slope of the MAP/SI response. Preliminary data suggest that BH elicited ~3-fold increases in MAPR, translating to a larger anterior and posterior CVR than during RB. If confirmed, these findings suggest that the sympathetic responses during breath-holding are larger than those during rebreathing across similar chemostimuli. This work has potential implications for understanding stroke risk in obstructive sleep apnea patients, who experience intermittent breath holds and increased sympathetic activation during sleep.

HS-11

NEUROVASCULAR COUPLING IS UNCHANGED DURING SITTING, STANDING OR WALKING: IMPLICATIONS FOR ACTIVE WORKSTATIONS

Dexter Merenick, Justine M. Doll, William G. Camden, Rosie A. Jones, Hope L. Guenard, Carli R. Mann, Joel D.B. Peltonen, Jack K. Leacy, Ken D. O'Halloran | Supervisor: Trevor Day
(Department of Biology, Mount Royal University)

Neurovascular coupling (NVC) is a phenomenon matching regional cerebral blood flow to neuronal metabolic activity. Improvements in NVC may underlie qualitative reports of improved cognitive performance using standing and active workstations. Little has been investigated pertaining to the potential physiological effects of sitting, standing or walking on NVC. We hypothesized that sitting, standing and low-intensity treadmill walking (2 mph) would increase NVC magnitude in a dose-dependent fashion.

We recruited 20 participants and instrumented them with an electrocardiogram (beat-by-beat heart rate; HR; bpm), finger photoplethysmography (mean arterial pressure; MAP; mmHg) and transcranial Doppler ultrasound to quantify posterior cerebral artery velocity (PCAv; cm/s) during sitting, standing and walking. The protocol consisted of a 3-min baseline (BL) and three x 30-sec standardized visual stimulus (VS) periods using a strobe light in each position. Individual responses were quantified and averaged through visually identified peak(s), time-to-peak(s), and mean PCAv response(s) during VS.

Baseline HR was incrementally higher in sitting, standing and walking (P<0.001), but MAP was unchanged (P=0.12). There were significant increases in peak and mean responses from BL in all positions during VS (P<0.001), confirming an NVC response. There were no differences in delta peak (P=0.47), time-to-peak (P=0.29) nor delta mean (P=0.76) NVC responses during VS, suggesting that NVC magnitude is unaffected by body position or low-intensity exercise. We conclude that reports of increased cognitive performance while using standing or active workstations are not related to NVC.

HS-12

CEREBRAL BLOOD FLOW PULSATILITY INDEX IS UNCHANGED DURING SUPERIMPOSED LOWER-BODY NEGATIVE PRESSURE IN HEAD-UP TILT IN ANTERIOR AND POSTERIOR CEREBRAL CIRCULATIONS

Tara Salloum, Anthony Marullo | Supervisor: Trevor Day
(Department of Biology, Mount Royal University)

Lower body negative pressure (LBNP) chambers can be utilized to experimentally-elicit reductions in blood pressure, cerebral blood flow (CBF) and associated symptoms of presyncope. Tolerance to LBNP is varied, however the underlying physiological responses affecting tolerance remains unclear. Pulsatility in CBF may affect LBNP tolerance, as more pulsatile flow may protect the delivery of oxygen to cerebral tissues in hypotension. We aimed to assess the pulsatility index (PI) in anterior and posterior cerebral circulations during LBNP in superimposed head-up tilt (HUT),

where gravitational-induced blood volume re-distribution augments volume unloading during LBNP.

We recruited 12 healthy male participants, and instrumented them in a 45° HUT-LBNP chamber. Participants were instrumented for heart rate (HR), mean arterial pressure (MAP), and middle and posterior cerebral artery velocity (MCAv, PCAv). All measures were recorded during baseline (BL) and during -50 mmHg LBNP exposure up to a maximum of 10-minutes (600s). Presyncope was defined as a 30% reduction in systolic blood pressure or onset subjective symptoms. We quantified all variables during BL and the final 30-sec of LBNP prior to presyncope. MAP, MCAv and PCAv PI was calculated as systolic-diastolic/mean.

MAP decreased from 84.8±11.3 (BL) to 76.2±14.7 mmHg (P<0.01) during LBNP, with associated reductions in mean MCAv from 52.1±15.0 to 44.3±14.5 cm/s (P<0.01), and mean PCAv from 35.5±12.6 to 29.0±9.9 cm/s (P<0.01) during LBNP. MAP PI was reduced from 0.76±0.2 to 0.59±0.02 (P<0.01) during LBNP. However, MCAv and PCAv PI were unchanged during LBNP (P=0.6 and P=0.9, respectively).

Our results suggest that although MAP and MAP PI were both reduced during LBNP at pre-syncope, with associated reductions in mean MCAv and PCAv, MCAv and PCAv PI remained stable with LBNP in HUT. These findings suggest that PI in CBF variables at the cardiac frequency are not related to LBNP tolerance in healthy men.

HS-01
PREVENTION OF CEREBRAL PALSY DURING THE PRENATAL PERIOD

Sarah Almas, Oriana Shaw | Supervisor: Jerome Yager
(Department of Medicine, University of Alberta)

Cerebral palsy (CP) is the most common motor impairment of childhood, and its prevalence has not decreased over the past several decades. Approximately 85-90% of initiating factors that cause CP occur during the fetal period, and premature birth is associated with over half of CP cases. Here, we hypothesize that antenatal prevention strategies minimize factors precipitating CP. Medline, PubMed and Cochrane Library from 2005 to 2020 were searched using the terms "prevent", "fetal", "neonatal", "perinatal", "infant*", "ped*", "antenat*", "prenat*", and "cerebral palsy" to identify human randomized control trials, meta-analyses and reviews. Primarily, magnesium sulphate (MgSO4), an inorganic salt with anti-inflammatory and antioxidant properties, was tested in several populations of pregnant women at risk of delivering their children early. Different dosing regimens were associated with varying outcomes for the child, but overall the use of MgSO4 was associated with significantly lower rates of CP in children when mothers were exposed to it during pregnancy. The most promising MgSO4 dosing regimen of 4-6 g loading dose and 1-2 g per hour maintenance infusion provided fetal benefit with minimal adverse effects. Standardized MgSO4 dosing regimens at institutions are recommended to provide protective effects to unborn children. Other interventions that showed promise in animal studies did not have enough supporting evidence for clinical use in humans, including melatonin, progesterone, creatinine, allopurinol, thyroid hormones, antibiotics, and corticosteroids. Further human studies to elucidate the risks and benefits of these promising antenatal therapies will help guide clinical practice and protect infants at risk of developing CP.

HS-02
ROLE OF SEX AND THE MICROBIOME IN PRODUCTION OF 'NATURAL' ANTIBODIES IN A MOUSE MODEL

Bushra Anjum, Ibrahim Adam, Jean Pearcey, Kesheng Tao, Bruce Motyka | Supervisor: Lori J. West
(Department of Biological Sciences, University of Alberta)

Purpose: ABO histo-blood group incompatibility is a barrier to performing solid organ transplants due to 'natural' preformed ABO antibodies. In humans, these natural ABO antibodies are produced around 6-months of age, however, the exact mechanism of production is not fully understood. It is hypothesized that natural ABO antibodies

may develop due to cross-reactivity with components of the gut microbiome. A better understanding of how ABO antibodies develop may have important implications for lifesaving ABO-mismatched transplantation.

Methods: An ABH glycan microarray was used to determine the isotype (IgM/IgG) and ABH subtype specificity (subtypes I-VI) of natural ABO antibodies in plasma (from tail-bleeds) of germ-free and conventionally-housed C57BL/6 (B6; females/males, n=10/10) and BALB/c (BALB; females/males, n=10/10) inbred mice, and Swiss Webster (SW; females/males, n=4/6) outbred mice.

Results: Anti-A antibodies were present in germ-free B6, BALB and SW mice at levels similar to conventionally-housed mice. At 4-weeks of age, IgG (but not IgM) anti-A antibodies were detected in both sexes at similar levels to older (12-week) female mice. Anti-A antibodies in males >8-weeks of age, remained mostly IgM. In females, anti-A antibodies were mostly IgG isotype at 4-weeks of age, mainly IgM isotype at 8-weeks of age, and then shifted to mostly IgG isotype by 12-weeks of age. Most natural anti-A antibodies, in germ-free or conventionally-housed mice, were specific to subtypes III/IV whereas antibodies specific to subtype II antigens were low/absent.

Conclusion: Detection of natural anti-A antibodies in germ-free mice and higher levels of natural anti-A antibodies in females vs males suggests a unique sex-dependent, alternative mechanism of natural ABO antibody production than cross-reactivity with gut microbiome antigens.

HS-04
UNDERSTANDING THE ROLE OF DDX1 EXPRESSION IN NEUROBLASTOMA RESPONSE TO TREATMENT

Jessica Bennett, Lei Li, Jack Wang | Supervisor: Roseline Godbout
(Department of Cell Biology, University of Alberta)

Neuroblastoma is a pediatric cancer originating from neural crest cells and is the most lethal extracranial solid tumour in children. High-risk neuroblastoma is often associated with amplification of the MYCN oncogene. DEAD box proteins are involved in modification of RNA secondary structure and have been implicated in cellular stress response. Previous research undertaken by the Godbout lab indicates that the DEAD Box 1 (DDX1) gene is co-amplified with the MYCN gene in about 50% of high-risk neuroblastomas. My hypothesis is that amplification of the DDX1 gene in neuroblastoma cell lines improves their survival following treatment with DNA damaging agents.

Neuroblastoma resistance to treatment was measured using the anchorage independence assay which measures the ability of single cancer cells to form colonies in semi-soft agar. While DDX1 knockdown had no effect on colony formation in cell lines treated with the microtubule-inhibiting chemotherapy drug vincristine, DDX1 knockdown resulted in increased resistance to ionizing radiation and etoposide in DDX1-amplified neuroblastoma cell lines. Based on my results, DDX1 may exert different cellular effects when present at basal levels compared to when overexpressed. In DDX1-amplified cell lines, co-amplification may lessen the detrimental effect observed by MYCN overexpression in high-risk neuroblastomas. We conclude that altering the levels of DDX1 may increase the efficacy of radiation and certain chemotherapy drugs used for the treatment of neuroblastoma, leading to a reduction in the mortality of infants and children diagnosed with high-risk neuroblastoma.

HS-05
INVESTIGATING THE ROLE OF DEXAMETHASONE ON IMMUNE REGULATION

Mai Huynh | Supervisor: Shokrollah Elahi
(Department of Biological Sciences, University of Alberta)

Although the immune system is a powerful tool for combating infections, excessive immune activation can elicit numerous long-term health complications calling for the need for medication with a potential target of modulating

immunoregulatory cells. Dexamethasone is a corticosteroid with a wide range of applications and is known for its anti-inflammatory and immunosuppressive effects. Futhermore, previous research by the Elahi lab indicated that newborns are enriched with immature red blood cells (CD71+ Erythroid Cells (CECs)) that actively suppress newborn immune systems, reducing excessive immune activation which could otherwise aggravate immune development. In this study, we aimed to investigate the role of dexamethasone on immune cells using a murine model. BALB/c littermate mice up to a week old and mice over 10-weeks-old were used for the experiments. Treated mice were injected with dexamethasone and control mice with PBS. To examine the effect of dexamethasone in the spleen and bone marrow, cells were isolated and used for immunophenotyping and in various functional assays. In comparison to control mice, we found that mice injected with dexamethasone displayed lower levels of CECs and increased levels of matured red blood cells (RBCs) in the spleen. In contrast, the bone marrow displayed higher levels of CECs and decreased RBCs. Both trends were consistent in neonatal and adult mice. Intriguingly, we observed that treated mice also had increased numbers of Ly6G and Ly6C single or double-positive cells in the spleen and bone marrow of both neonatal and adult mice, with a higher effect observed in neonatal mice. In addition, isolation of these expanded cells and co-culture with responder T-cells showed an enhanced proliferation effect in vitro. Our findings present an investigation into the role of dexamethasone on immune cells, giving further insight into its numerous diverse impacts on various immunoregulatory cells.

SESSION B1 | 9:15 AM - 12:00 PM

BIOCHEM-03

CHARACTERIZATION OF AN APTAMER FOR AFLATOXIN B1 AND SUBSEQUENT APTASENSOR DESIGN.

Alana Loutan, Alex Beke | Supervisor: Nina Bernstein
(Department of Biological Sciences, MacEwan University)

Aptamers are nucleic acid-based ligand binding molecules that are capable of strong and specific binding to small molecule, protein, or whole cell ligands. These versatile nucleic acids can be paired with visualization techniques to create sensors aptly named aptasensors. Our research project is aimed at developing a DNA-based aptasensor for the detection of aflatoxin B1 (AFB1) by pairing it with DNAzyme. For the purposes of our project, DNAzyme can be thought of as a DNA sequence that will fold into a G-quadruplex to catalyze an oxidation reaction ultimately producing a green colour from colourless reagents. To properly design our aptasensor, we first carried out characterization experiments. These included a native gel to test for conformational change, UV absorption spectra, and DMS probing. Our native gel and UV absorption spectra were too low in resolution to give conclusive results with respect to the conformational change. DMS probing is a type of fingerprinting experiment that allowed for the elucidation of AFB1 binding sites on the aptamer. An end-labeling technique was required for the DMS probing. Since our university is not equipped for radioactive end labeling, we decided to develop a modular fluorescent end labeling technique. This technique involved a 5'-fluorescently labeled "probe" molecule (14 mer) that is ligated to the aptamer by use of an adaptor oligonucleotide (complementary to both the probe and 3' end of the aptamer), T4 PNK and T4 DNA ligase. Currently the aptamer is being characterized and eventually aptasensor design will be attempted. The goal is to design a same-strand split DNAzyme aptasensor though, due to time constraints, testing of this aptasensor will not be possible during this project.

BIOCHEM-01:

GENOME MINING FOR THE DISCOVERY OF CIRCULAR ANTIMICROBIAL PEPTIDES

Lara Flanzbaum | Supervisor: Jeella Acedo
(Department of Chemistry and Physics, Mount Royal University)

Bacteriocins are ribosomally synthesized antimicrobial peptides produced by a variety of bacterial species. A class of bacteriocins known as circular bacteriocins is characterized by their cyclic peptide backbone that confers high stability against pH variations, proteolysis, and thermal stress, making them excellent compounds for antimicrobial applications. In this study, we performed genome mining to search for novel members of subgroup I circular bacteriocins using the transporter protein sequences associated with characterized circular bacteriocins as query sequences. By performing pBLAST and RODEO analysis, a total of 142 putative subgroup I circular bacteriocins were identified. A sequence similarity network (SSN) of the bacteriocin amino acid sequences was then created, wherein similar bacteriocins were grouped together in clusters. Some sequence clusters did not have any characterized representative members and future research may be directed towards the characterization of members of the said groups. Searching for new bacteriocins is valuable especially during a time of increasing occurrence of antimicrobial resistance, as bacteriocins are considered as promising alternatives to traditional antibiotics.

BIOCHEM-04

GENOME MINING AND ISOLATION OF BACTERIA-DERIVED ANTIMICROBIALS

Leah Lussier, Daniel Major, Lindsay Leahul, Jhoseling Garcia, Susan Ross Hamilton | Supervisor: Jeella Acedo
(Department of Chemistry, Mount Royal University)

Bacteriocins are a highly heterogeneous group of antimicrobial peptides produced by a wide array of bacteria. These peptides have commercial applications in food preservation and livestock industries, with potential as next-generation antimicrobials. The focus of this project is on leaderless bacteriocins, which are defined by the absence of an N-terminal leader peptide and the typical post-translational modifications present in other bacteriocin classes. Through genome mining, we identified 75 putative leaderless bacteriocins based on homology using the precursor peptide sequences of experimentally validated leaderless bacteriocins. We selected two of these peptides, which we named VigA and MitA, and used a heterologous Escherichia coli BL21 expression system to produce His6-SUMO tagged peptides. VigA and MitA were purified using nickel affinity chromatography, and the SUMO tag was cleaved using SUMO protease. Purification using high-performance liquid chromatography is underway. The identity of the purified peptides will be verified using MALDI-TOF mass spectrometry and the bioactivity against a suite of organisms will be investigated.

BIOCHEM-10

IDENTIFYING THE INTERACTIONS BETWEEN SHEWANELLA-LIKE PROTEIN PHOSPHATASE 1, AND ITS SPECIFIC SUBSTRATE, CALVIN CYCLE PROTEIN 12 IN ARABIDOPSIS THALIANA

Lana Wong, Jayde Johnson | Supervisor: Gregory Moorhead
(Department of Biological Sciences, University of Calgary)

Protein phosphorylation is the most common post-translational modification and is essential in mediating most cellular functions in all organisms. This reversible covalent modification has a wide variety of effects ranging from changes in the protein's localization and activity, to the hiding or revealing of binding pockets. These changes result in the activation or deactivation of the protein itself, as well its downstream signalling pathways. In plants, reversible protein phosphorylation plays a central role within the chloroplast, regulating processes such as photosynthesis and starch metabolism. The addition of a phosphoryl moiety is catalyzed by protein kinases, whereas the removal is catalyzed by protein phosphatases. Shewanella-like phosphatases (SLP) are a recently characterized phosphatase belonging

to a subclass of the serine/threonine-specific phosphoprotein phosphatase (PPP) family. There are two SLPs in Arabidopsis thaliana (At): AtSLP1 and AtSLP2, which are localized in the chloroplast and mitochondria, respectively, with AtSLP1 being the focus of this project. Through a quantitative mass spectrometry based phosphoproteomics study carried out by previous members of the Moorhead Lab, putative substrates of AtSLP1 were identified, many of which contained an unusually high abundance of acidic amino acid residues surrounding the phospho-sites. One of these substrates is Calvin cycle protein 12 (CP12), which plays a role in the thioredoxin-mediated regulation of the Calvin-Benson cycle. To better understand the functionality of these acidic residues, a phospho-mimetic substrate extension was added to SLP1 in order to circumvent any concentration problems or need for regulatory subunits, allowing it to wrap around and bind in the active site of SLP1. The phospho-mimetic residue enhances the binding of CP12 to the SLP1 active site, inherently increasing the stability of SLP1 and the possibility of observing enzyme-substrate interactions from crystallography.

BIOCHEM-02
BIOPHYSICAL AND STRUCTURAL CHARACTERIZATION OF SP1-ZINC FINGER DOMAIN AND HEPATITIS B VIRUS PROMOTER INTERACTION

Nic Jujihara, Gerardo Balderas Figueroa, Maulik D. Badmalia | Supervisor: Trushar Patel
(Department of Biochemistry, University of Lethbridge)

Hepatitis B virus (HBV) is a deadly human virus that is responsible for nearly 1m deaths annually. Despite the availability of effective vaccines, approximately 250M individuals globally are chronically infected with HBV. It contains a relaxed circular DNA genome which upon infection forms a covalently closed circular DNA – the chief cause of relapse of infection if the treatment is stopped. The virus relies on human proteins for its replication. One such protein is known as the Specificity protein-1 (Sp-1), which is an important human transcription factor. Sp-1 interacts with all four promotor regions of the HBV genome, and the interaction is essential for viral replication. Functionally Sp-1 is divided into six domains, one of which is the Zinc finger (ZnF) that is essential for DNA binding. We recently demonstrated that one of the Sp-1 binding sites on HBV DNA forms a G-quadruplex (G4) structure. Our next main objective is to understand the recognition events between human Sp-1 and HBV DNA G-quadruplex. As a first step, we expressed the Sp-1 ZnF domain in E. coli and purified it using affinity and size-exclusion chromatography. Next, we prepared G-quadruplexes in vitro based on the HBV promoter region G-rich sequence. We sought to verify the interaction between Sp-1 ZnF domain and the synthetic G-quadruplex using biophysical techniques such as microscale thermophoresis. Furthermore, we seek to determine the solution structure using small-angle X-ray scattering. Insights into the Sp1 ZnF – HBV G4 complex could provide a platform to develop inhibitors that can prevent this interaction and thereby, inhibit HBV replication.

BIOCHEM-05
STUDYING TRNA BINDING AND MODIFICATION BY THE ENZYME TRMB
Kieran Meadows, Sarah Schultz | Supervisor: Ute Kothe
(Department of Chemistry & Biochemistry, University of Lethbridge)

Transfer RNAs (tRNAs) are the "delivery trucks" providing the right building blocks during protein synthesis in all organisms. All tRNAs undergo many chemical modifications, with more than 100 different modifications across all domains of life, which are critical for tRNAs to function. These modifications are carried out by enzymatic proteins, some of which are highly studied, but many are still not understood in their action. For example, comparatively little is known about the TrmB protein found in bacteria. This protein is responsible for introducing a 7-methlyguanosine in the variable arm of several tRNAs, potentially playing a role in promoting tRNA stability.
This study aims to understand how the TrmB protein recognizes and binds to the tRNA substrate. To this end, three amino acids were selected to be altered through site-directed mutagenesis as we predict that these amino acids play critical roles during tRNA recognition and methylation. Subsequently, the TrmB variant proteins were overexpressed and successfully purified through affinity chromatography as well as size exclusion chromatography. In the future, the TrmB variant enzymes' binding interaction will be tested with fluorescently labelled tRNA substrate in order to identify

the kinetics and mechanism of tRNA recognition by TrmB.

In summary, this project will identify critical molecular determinants in TrmB that help this enzyme to specifically recognize tRNAs for modification. By better understanding how and why tRNAs are modified in all organisms, we will gain fundamental insight into protein synthesis with possible future applications in drug design and bioengineering. "

BIOCHEM-06

TOWARDS UNDERSTANDING FLAVIVIRAL GENOME CYCLIZATION

Sean Park, Tyler Mrozowich, Michael Wolfinger | Supervisor: Trushar Patel
(Department of Chemistry and Biochemistry, University of Lethbridge)

Family Flaviviridae is composed of pathogenic viruses such as Dengue, West Nile, Zika and Japanese encephalitis virus (JEV). Flaviviral genome cyclization involving their 5' and 3' terminal regions (TR), which are conserved across the various members of this family, has been shown as a critical step in viral replication. However, the exact biochemical and biophysical basis underlying the interaction is yet to be elucidated. Therefore, we selected JEV, which is responsible for infecting ~68,000 humans annually with over 25% of cases resulting in death, to investigate the interactions between its 5' and 3' TR. First, we performed bioinformatics analysis of JEV genomes to identify the 5' and 3' TRs that were predicted to interact with each other with high affinity. Next, we designed and purified multiple RNA transcripts for both the 5' and 3' TRs through using in vitro transcription and chromatography. With the highly purified RNAs, we performed interaction studies using microscale thermophoresis (MST). The results demonstrated that the 5' TR interacted with the 3' TR. We also performed light scattering analysis using a combination of biophysical techniques (SEC-MALS-DLS-RI) to optimize the conditions for future biophysical experiments to obtain insights into the 5' – 3' TRs complex. Ultimately, our multidisciplinary work will provide detailed understanding of Flaviviral genomic cyclization.

BIOCHEM-07

LONGITUDINAL TIME-SERIES ANALYSIS OF THE EFFECTS OF LONG-DURATION SPACE TRAVEL IN MALE AND FEMALE NASA ASTRONAUTS USING A 1H-NMR-BASED METABOLOMICS APPROACH

Julia Stroud, Micheal Gale, Tony Montina, Scott Smith, and Sara Zwart | Supervisor: Gerlinde Metz
(Department of Chemistry and Biochemistry, University of Lethbridge)

Metabolomics, an approach which investigates the terminal metabolites of physiological pathways, takes into account the dynamic state of the human body and allows for the identification and quantification of the metabolic outputs linked to upstream regulation by stress. Space flight provides a unique opportunity to investigate longitudinal profiles of metabolic changes linked to physiological and psychological stress and the current study presents the first attempt to address this topic. Development of accurate methods for the assessment of metabolic changes during an astronaut's mission would allow for better monitoring of health throughout missions and the development of countermeasures to reduce the risk of lifelong adverse consequences following spaceflight. In this study, we investigated the metabolic perturbations of male (n=40) and female (n=11) NASA astronauts using proton nuclear magnetic resonance (NMR) spectroscopy on blood serum to examine sex-specific metabolic changes at various time points throughout the astronaut's missions, as well as the metabolic effects of long-duration (4-6-months) space travel. Univariate, multivariate and machine learning analyses were used to identify metabolites and pathways that provide insight into sex differences and the effects of long-duration space travel. The pathways that were identified to be uniquely affected in the male astronauts were branched chain amino acid degradation, and aminoacyl-tRNA biosynthesis. In contrast, the metabolic pathways that were determined to be uniquely affected in the female astronauts were the tricarboxylic acid cycle (TCA); glycerolipid metabolism; glycine, serine and threonine metabolism; cysteine and methionine metabolism; pantothenate and CoA biosynthesis; and arginine and proline metabolism. These findings give insight into the perturbations in carbohydrate and amino acid metabolism, protein synthesis, and the immune effects that result from space travel.

BIOCHEM-08

INVESTIGATING THE INTERACTION BETWEEN PDCD4 AND EIF3F WITH RESPECT TO TRANSLATION REGULATION

Katrina Taylor | Supervisor: Nehal Thakor
(Department of Biological Sciences, University of Lethbridge)

Programmed cell death 4 protein (PDCD4) is a well studied tumor suppressor gene that is found to be decreased in many types of cancer; including, glioblastoma multiforme and colorectal cancer. PDCD4 is known to mediate the anti-apoptotic effects of X chromosome-linked Inhibitor of Apoptosis (XIAP) and B-cell lymphoma extra-large (Bcl-xL) through IRES mediated translational initiation regulation. Eukaryotic Initiation Factor 3F (eIF3F) is also a tumor suppressor protein that acts as a negative regulator of translation and has also been found to be downregulated in most human tumors. PDCD4 and eIF3F have been found to interact with each other in vitro and in cellulo, possibly affecting translation initiation and therefore cellular survival. This study investigates how altered levels of PDCD4 and eIF3F both independently and coupled affect levels of the other and of Bcl-xL . A partial knockdown of eIF3F showed decreased levels of PDCD4 and increased levels of Bcl-xL while a partial knockdown of PDCD4 showed decreased levels of eIF4F. This research highlights the interactions between PDCD4 and eIF3F and can potentially provide mechanistic information into how PDCD4 regulates non-canonical translation initiation.

BIOCHEM-09

LEARNING WHAT IT TAKES TO BE ESSENTIAL IN RIBOSOME SYNTHESIS: A MUTAGENESIS STUDY OF SNR30 RNA FUNCTIONALITY

Scott Tersteeg, Josh Friesen and Daniel Rocca | Supervisor: Ute Kothe
(Department of Chemistry and Biochemistry, University of Lethbridge)

Ribosomes are the protein factories of all cells. The formation of ribosomes is critical to cellular growth and a potential target for future cancer therapies. All cancerous cells are characterized by an upregulation of ribosome biogenesis, which depends on increased activity of the factors required to process the precursor ribosomal RNAs (rRNA) [1]. My project is investigating the essential nucleolar RNA snR30 from baker's yeast, a homologue of human U17 RNA, with the goal to further understand why and how snR30 is required for the formation of the small ribosomal subunit, specifically the processing of rRNA from a long precursor to its mature form. Possibly, snR30 may help the rRNA to fold and/or it may recruit other proteins that specifically cleave rRNA [2].
To better understand how snR30 sequence and structure contributes to its function in ribosome biogenesis in yeast, I have introduced 10 mutations in snR30 at specific sites that are hypothesized to help with rRNA folding or to interact with proteins that are required for rRNA processing. The mutated snR30 was transformed in a yeast strain where the chromosomal snR30 gene can be repressed. The growth phenotype of the cells expressing mutant snR30 will be compared to wild type yeast to determine the effects of the mutation. No growth of the yeast colony will indicate the mutated nucleotide was essential to ribosome biogenesis. A colony that shows significantly reduced growth when compared to the wild type indicates reduced functionality of the snR30 via inefficient binding to proteins or the rRNA. Future studies will deduce the molecular defect of the different mutations on processing the rRNA. Taken together, my research will contribute to our understanding of how ribosomes are synthesized with the help of RNA and protein assembly factors.

[1]:   https://doi.org/10.1038/nrc.2017.104
[2]:   https://doi.org/10.3390/cells9102195"

SESSION B2 | 9:15 AM - 12:00 PM

BIOL-05

EFFECTS OF INTERANNUAL VARIABILITY IN SEED PRODUCTION OF 5-NEEDLED PINES ON NUTCRACKER CACHING IN BURNS

Evan Buist | Supervisor: Vern Peters
(Department of Biology, The King's University)

Whitebark pine (Pinus albicaulis) and limber pine (Pinus flexilis) are endangered species that rely on fire for regeneration to varying degrees. The Clark's nutcracker, a mutualist of both species, plays a crucial role in their ecology through the dispersal and caching of their seeds on fires, particularly in mast seed years. We tested whether nutcracker activity differed between mast (2018) and non-mast years (2019), on the 2009 North Saskatchewan Fire. We examined three sites for each species, at varying distances into the fire to determine whether nutcracker activity varied between unburned seed sources, and burned sites. We used Ravenpro and Kaleidoscope acoustic analysis software to identify nutcracker calls and build preliminary song classifiers to detect and quantify nutcracker activity. Nutcracker calls were manually observed and annotated as call bursts using spectrogram analysis. Preliminary manual observation suggested that nutcracker activity was higher in non-mast years, with a 64% increase in call bursts/hour. However, we found significant observer differences, with 45% under detection in the mast year analysis. This led to an increased focus on standardizing audio observation across many observers. After assigning a correction factor to make up for the under detection in the 2018 mast year, it was found that the mast year had 27% more nutcracker call bursts/hour, indicating nutcracker activity was higher during the seed dispersal period of a good cone crop year. Our findings suggest that nutcrackers are preferentially caching the seed in mast years. However, the uncertainty in detecting nutcrackers using acoustic classifiers under windy and rainy conditions is still limiting our ability to detect differences between activity on mast and non-mast fires. A proper understanding of nutcracker use of burned habitat is important to applying fire management in recovery actions for each of these endangered pines.

BIOL-08

ASYMMETRICAL BINDING OF HSP90 COCHAPERONES AND ITS EFFECTS ON COCHAPERONE CYCLING

Daniel Clark | Supervisor: Annerieke Wolmarans
(Department of Natural Sciences, The King's University)

Hsp90 is a ubiquitous homodimeric molecular chaperone that matures and activates numerous client proteins, many of which are associated with the progression of diseases such as cancer, Alzheimer's disease and Parkinson's disease. Hsp90 matures clients by undergoing a poorly understood ATPase cycle which is regulated by various cochaperone proteins. Cochaperone proteins bind to one or more of Hsp90's domains in a sequential, ATP-dependent manner to regulate its ATPase cycle. Firstly, the Sti1 cochaperone recruits client proteins to Hsp90, inhibiting its ATPase activity. Sti1 is then displaced by the cooperative action of co-chaperones Aha1 and Cpr6, leading to the hydrolysis of ATP and release of the mature client. Despite there being two binding sites for every cochaperone on the dimeric Hsp90, recent studies show that Hsp90 is regulated asymmetrically; cochaperone binding on one of the two subunits of Hsp90 results in conformational changes that alter binding properties elsewhere on the chaperone. We are interested in investigating the asymmetric binding of Sti1, Aha1 and Cpr6 that promote cochaperone cycling to elucidate the mechanism of Sti1 displacement. To explore asymmetry, we used well-established protocols to generate heterodimers harboring characterized Hsp90 mutants to promote Aha1 binding to the opposite subunit to which Sti1 and Cpr6 binds to. Utilizing Michaelis–Menten kinetics, we measured the ATPase activity of these Hsp90 heterodimers in a cycling reaction and our results show that Sti1 can be cooperatively displaced by Aha1 and Cpr6 to a similar degree as wildtype Hsp90 homodimers. Surprisingly, we discovered that Sti1

was unable to effectively inhibit the Hsp90 heterodimers when it bound to the non-hydrolyzing subunit. Our work highlights that asymmetric ATP binding can affect the action of cochaperones and reveals the importance of further research into the asymmetrical mechanisms of cochaperone regulation.

BIOL-20
THE EFFECTS OF BETA-CYCLODEXTRIN ON ZEBRAFISH LENS CLARITY

Jack Lacroix | Supervisor: Heather Prior
(Department of Biology, The King's University)

Zebrafish can act as an excellent model organism for current eye research. The zebrafish lens has proteins similar to ones present in mammalian lenses, in which cataract formation may occur by certain protein aggregation events. The cataract induction method performed in this research used oxidative stress to aggregate lens proteins. Beta-Cyclodextrin (BCD) is a known drug delivery molecule that has some potential for use as an antioxidative agent. This study aimed to determine how effective BCD was as an agent for reducing lens cloudiness in zebrafish. Zebrafish were unilaterally induced with cataracts and then euthanized to remove both healthy and cataract lenses. Each lens was placed into different concentrations of BCD, and photos were taken every 24 hours to observe the lens clarity over a total of 96 hours. Lenses were graded by a single-blind assessment of photos, using a 1-4 cataract severity scale. The results showed that the most effective use of BCD occurred at 200uM concentration after 48 hours, when the clarity of both the healthy and cataract lenses improved by a full grade point on average. This study shows that BCD might not only be an effective drug delivery molecule, but also a potential treatment that prevents protein aggregation in the lenses of zebrafish.

BIOL-29
ECHINOCOCCUS MULTILOCULARIS PREVALENCE AND RISK FACTORS FOR INFECTION IN DOMESTIC DOGS IN EDMONTON ALBERTA.

Emilie Porter | Supervisor: Darcy Visscher
(Department of Biology, The King's University)

Echinococcus multilocularis is a trophically transmitted parasitic helminth and is an emerging zoonotic tapeworm of growing concern according to the World Health Organization. Normally requiring two mammalian hosts to complete its lifecycle, Echinococcus moves through small rodents and wild canids. Domesticated dogs can also act as definitive hosts. Definitive hosts can incidentally interact with humans and facilitate the transmission of this parasite in synanthropic environments. Echinococcus multilocularis is the etiological agent for Alveolar Echinococcosis in humans, which is difficult to diagnose and has a case mortality rate of >90% when left untreated. Alveolar Echinococcosis has historically been rare in North America, however since 2013, at least fourteen diagnoses have been confirmed in Edmonton, Canada. This study was completed in Edmonton to determine the prevalence of Echinococcus multilocularis infection in domestic dogs. From May – August 2020, faecal samples and corresponding behavior risk surveys were collected from 775 dogs in urban off-leash parks within Edmonton City limits. Q-PCR was used in order to extract and amplify Em infection. It was determined that 0.12% (0-0.99%) of samples tested positive for Echinococcus Multilocularis (1/775). Overall, these findings determine that Echinococcus multilocularis is present in urban off-leash parks and the overlap of wild and domestic canids may enhance zoonotic infection.

BIOL-10

PARASITES AND STABLE ISOTOPES: THE POTENTIAL FOR NEW TAXON-SPECIFIC DISCRIMINATION FACTORS

Kaegan Finn, Karling Roberts | Supervisor: Mark Poesch
(Department of Renewable Resources, University of Alberta)

Using stable isotopes to study food webs has become a common practice in aquatic ecology. Until recently parasites were largely omitted from these analyses, despite the known importance of parasites in food webs. Additionally, when parasites were included in food web studies, long- standing assumptions about the enrichment of 15N in consumers relative to their resources often placed parasites in a trophic level above their hosts. However, recent literature has shown that unlike consumers to prey, parasites do not reliably exhibit enrichment in 15N with respect to their hosts. This is particularly true of parasites in the class cestoda, which tend to be depleted in 15N relative to their hosts. To date, much of the research showing this relationship has been conducted in Europe. To determine if this trend holds true in Alberta, I analyzed stable isotope ratios of nitrogen and carbon in cestode parasites and their fish hosts across four lakes in northern Alberta. In the future, nitrogen and carbon isotope values of host and uninfected fish will be compared to determine if infection impacts the trophic ecology of host fish. Results from this study will expand the geographic range of cestode parasite isotope studies considerably and improve our understanding of how stable isotopes can be used to effectively include parasites in food webs.

BIOL-12

THE MOLECULAR BASIC OF CAROTENOID BIOSYNTHESIS IN CLEOMACEAE

Matthew Gerun, Brandi Zenchyzen | Supervisor: Jocelyn Hall
(Department of Biology, University of Alberta)

Angiosperms are a remarkably successful and diverse clade of organisms, and much of this is due to their defining feature, the flower. Floral traits may differ dramatically even between closely related species, and minor phenotypic differences can be evolutionarily consequential. Petal colour is a particularly important feature, playing a primary role in pollinator attraction, and hence reproduction. Carotenoid and anthocyanin pigments are the primary determinants of floral colour. Cleomaceae, sister to the more extensively researched and utilized Brassicaceae, has morphologically diverse, monosymmetric flowers, differing greatly from the uniform flowers of its sister family. The diversity in colour and form in Cleomaceae makes it ideal for this study. The lability that exists in the carotenoid biosynthetic pathway allows for different pigments to be produced, or for the production to cease, with minor genetic changes. We are investigating the differential production of petal carotenoids within and between four members of Cleomaceae. Using transcriptomic analysis, we are analyzing the differential gene expression in petals to develop an understanding of how carotenoids are produced in adaxial and abaxial petals of the same species that often differ in decoration, and between different species of the family. Data is still preliminary (COVID-19 has been a handicap in the timeline of this project), but my aims are to identify the location in the carotenoid biosynthetic pathway where pigment production ceases in white petaled species (G. gynandra), genes upregulated in the adaxial petals where there are large yellow spots (S. hirta), and genes upregulated in yellow flowers (A. viscosa, C. violacea). Of interest is the evolutionary, ecological, and systematic context that diverse pigment production occurs in, and comparing multiple members of the family allows for insight into where and why carotenoid production differs and the biological relevance of these changes.

BIOL-22

DISENTANGLING THE WORM: A POPULATION-LEVEL GENETIC ASSESSMENT OF A SNAIL SYMBIONT

Robert Lu, Brooke McPhail, Heather Proctor | Supervisor: Patrick Hanington
(Department of Biological Science, University of Alberta)

Chaetogaster limnaei is a species of oligochaete worm obligately symbiotic with freshwater snail hosts, with apparently cosmopolitan distribution. Two ecotypes are recognized in scientific literature: the external C. limnaei limnaei, which appears to be commensal or even mutualistic, and the endosymbiotic (potentially parasitic) C. limnaei vaghini, which feeds off liver tissues. However, it is unknown how these two ecotypes relate to one another genetically. Developments in molecular genetics have opened new ways to analyze structures of metapopulations, potentially revealing "cryptic species" only identifiable through genetic sequencing. The cytochrome oxidase subunit I (COI) gene in mitochondria is particularly useful for differentiating animal species, and in this case, was utilized to elucidate the genetic landscape of the Canadian C. limnaei metapopulation. DNA was extracted using column-based techniques from 187 C. limnaei worms, representing both ecotypes, and 15 Canadian waterbodies from Alberta, BC, New Brunswick, & Manitoba. COI sequences from each worm were aligned, focusing on the "Folmer" region of the gene; this alignment was used to construct a phylogenetic tree, assessed using bootstrap analysis. Pairwise comparisons of COI sequence similarities revealed two distinct clades (C1 & C2), with ~14.57% sequence divergence; C2 showed 4 subclades, differentiated by ~3.00% on average. From this, it was determined that C1 and C2 can be considered distinct species, while all four C2 subclades form distinct subspecies. Analysis of geographical isolation-by-distance effects (IBD) using a Mantel test revealed high IBD for C1 and C2 subclade 2,1. Between ecotypes, genetic differentiation was insignificant, indicating high phenotypic plasticity.

BIOL-40

OLFACTORY IMPRINTING OF BETA-PHENETHYL ALCOHOL IN ZEBRAFISH

Patricia Ann Villarama | Supervisor: Keith Tierney
(Department of Biological Sciences, University of Alberta)

Experiences as juveniles can shape behaviour of animals in adulthood. During a brief sensitive period in early animal development, long lasting memories of stimuli found in the environment can be made through a process known as imprinting. One of the most common stimuli found in aquatic environments are odorants that drive fish to perform ecologically important behaviours such as predator avoidance, foraging, migration and mating. We used a popular vertebrate model, the zebrafish (Danio rerio), to determine if they can imprint to olfactory cues and whether this can influence olfactory behaviour when as adults. We used the two odorants beta-phenethyl alcohol (beta-PEA) and kin odour. Larval zebrafish from 0.5 to 0.7 dpf were exposed to either beta-PEA or kin odour and afterwards were reared in an environment devoid of the odours until adulthood where we determined if the early exposure of the odorants influenced their adult behaviour using an avoidance attraction trough. We demonstrated imprinting of beta-PEA by showing that adult zebrafish that encountered beta-PEA as larva showed attraction to beta-PEA while control fish that did not encounter beta-PEA as larva were indifferent to beta-PEA. Exposing zebrafish to kin odour during development did not result in imprinting but control fish showed a wide distribution of attraction, avoidance and neutral behavioural response while fish exposed to kin odour during rearing showed mostly attraction. In conclusion, we demonstrated that zebrafish can imprint to olfactory cues, at least to beta -PEA, which in turn can influence their behavioural response to the odour when as adults.

BIOL-43

MAPPING CEREBRAL ABNORMALITIES USING TEXTURE ANALYSIS IN ALS WITH T2-FLAIR MRI: A MULTICENTER STUDY

Andrew Wu, Daniel Ta, Adam Elamy, Pedram Parnianpour, Lawrence Korngut, Angela Genge, Lorne Zinman, Annie Dionne, Michael Benatar, Robert Welsh | Supervisor: Sanjay Kalra
(Department of Biology, University of Alberta)

Background: Amyotrophic lateral sclerosis (ALS) is a fatal neurodegenerative motor neuron disease. Diagnosis is lengthy due to the lack of reliable neurodegenerative biomarkers. Having shown significant changes in the motor regions compared to controls, a voxel-wise approach of MRI FLAIR sequences can provide further insight. This project assesses the potential of voxel-based texture analysis on FLAIR as a quantitative marker for cerebral changes in ALS cross-sectionally and longitudinally.

Methods: A total of 154 subjects comprised of 81 patients and 73 controls from the Canadian ALS Neuroimaging Consortium (CALSNIC) were included. Whole-brain texture maps of normalized FLAIRs were calculated for every subject. Statistical analysis included group-level comparisons, voxel-wise regressions, and voxel-wise ROC at baseline and a longitudinal linear mixed model on the patient group.

Results: Statistical analyses showed significant areas of differences in the motor regions. Areas of high discriminatory ability were identified in the white matter bodies. Voxel-wise correlations corroborate the findings of the cross-sectional tests. Longitudinal changes were seen in the frontotemporal regions.

Conclusion: Highly spatially specific results suggest a promising future for voxel-wise texture analysis of FLAIR in ALS. Significant clusters in motor and cognitive regions align with current findings on ALS histopathology. Further studies that focus on the individual application of voxel-wise FLAIR texture could fulfill its powerful diagnostic potential.

BIOL-06

ASSESSING NATURAL SOURCES OF ETHANOL IN WILD PRIMATE FOODS: TESTING KEY PREDICTIONS OF THE DIETARY EXPOSURE HYPOTHESIS

Julia Casorso, Suheidy Romero Morales, Matthew Carrigan | Supervisor: Amanda Melin
(Department of Anthropology and Archaeology & Department of Biological Sciences, University of Calgary)

Humans and African great apes have a 40-fold higher efficiency for metabolizing ethanol relative to most other mammals, due to a shared genetic mutation. The ecological and evolutionary foundations of this trait currently remain unresolved. Although human-directed ethanol fermentation began 12,000 years ago, ethanol also occurs naturally in fruits and nectars. However, we have a poor understanding of the relative amounts and sources of variation of ethanol in these wild sources. The dietary exposure hypothesis posits that increased exposure to ethanol in ripe fruits selected for efficient ethanol metabolism in our last common ancestor with African great apes. My research seeks to test key predictions this hypothesis by studying ethanol concentrations in fruits from primate habitats around the world. Using a newly developed ethanol analysis system, we measured the ethanol content in varying ripeness stages of wild fruits collected at a primate field site in Costa Rica. We also sampled a variety of commercial fruits (purchased in Canada) to test potential factors contributing to variation in ethanol production. We found that ethanol production occurred in 66% of the 61 wild fruit species and 57% of the 14 commercial fruit species tested. Ethanol production in commercial fruits was greater at all ripeness stages and ranged higher (up to 4.22%) compared to wild fruits (up to 3.13%). Notably, we demonstrated that ethanol production follows a parabolic trend across time as fruits ripen, which frugivorous primates may use as a cue to optimize foraging decisions. Overall, this research marks the start of a growing global dataset that will provide new data on variation in fruit ethanol content. This knowledge will contribute to understanding the selection pressures that favoured efficient ethanol metabolism in the human lineage, as well as dietary adaptations in frugivorous mammals more broadly.

SESSION B3 | 9:15 AM - 12:00 PM

BIOL-02

THE IMPACT OF ASSUMPTIONS ABOUT PREVALENCE ON MODELS OF SUITABLE HABITAT FOR LONG-TOED SALAMANDERS IN SOUTH-WESTERN ALBERTA.

Jayna Bergman | Supervisor: Julie Lee-Yaw
(Department of Environmental Sciences, University of Lethbridge)

Amphibians are experiencing global declines, making it imperative to both inventory populations and to understand the factors that shape species' distributions. Species distribution models (SDMs) are a potentially useful tool in this regard, but model parameterization requires care as modeling decisions can impact results. This study tests the effects of assumptions about species prevalence when generating species' distribution models with the widely-used software, Maxent. We focus on the long-toed salamander (Ambystoma macrodactylum), a species of Special Concern in Alberta. Models were built using locality records from across the species' range and spatial data pertaining to climate. We varied the prevalence setting in Maxent from 0.4 to 0.7 and examined the impact on the predicted distribution of suitable habitat for long-toed salamanders at the edge of their range in south-western Alberta. In addition to internal validation, we used independent locality records from Waterton Lakes National Park (WLNP) to validate the models. Increasing prevalence resulted in both higher values of suitability and greater prediction of suitable habitat to the east of the species' current range. Independent AUC scores ranged from 0.5985 to 0.6667, with the model with a prevalence setting of 0.6 outperforming the others. These results indicate that assumptions about prevalence can have dramatic impacts on modeled distributions and habitat suitability scores. For long-toed salamanders, setting prevalence to 0.6 results in models that do a reasonable job of predicting independent data, demonstrating the value of using independent data to help optimize model settings.

BIOL-09

EFFECTS OF MATERNALLY DEPOSITED 1,2,5,6-TETRABROMOCYCLOOCTANE (TBCO) ON EARLY LIFE STAGE DEVELOPMENT AND REPRODUCTION IN JAPANESE MEDAKA (ORYZIAS LATIPES)

Chloe Devoy | Supervisor: Steve Wiseman
(Department of Biology, University of Lethbridge)

Brominated flame retardants (BFRs) are added to a variety of flammable products to increase their fire resistance. BFRs can leach from materials into aquatic ecosystems where they can bioaccumulate, biomagnify and induce toxicity in organisms. 1,2,5,6-tetrabromocyclooctane (TBCO) is an emerging BFR that is a potential replacement for the widely-used BFR, hexabromocyclododecane (HBCD). Little is known about effects of TBCO on aquatic organisms. In a previous study, exposure of zebrafish (Danio rerio) embryos to waterborne TBCO caused developmental toxicity. In another study, dietary exposure to TBCO impaired reproduction of Japanese medaka (Oryzias latipes). During fish development, embryos can be exposed to the same effective internal concentration as the maternal organisms from which the eggs originated. Effects of maternally deposited TBCO on fish development and reproduction have yet to be studied. The objective of this study is to determine the effects of maternally deposited TBCO on fish development and reproduction in Japanese Medaka. Sexually mature fish (F0) were fed either a control, low (100 µg/g) or high (1000 µg/g) dose of TBCO spiked fish food for 21 days (N=40). On days 15 and 20 of the exposure, embryos were collected to assess developmental toxicity caused by maternally deposited TBCO and grown to reproductive maturity to assess reproductive performance. Exposure to dietary TBCO showed trends of decrease in fertility, fecundity, and GSI in the F0 generation. In the F1 generation, embryos showed concentration dependent trends of increased functional mortality, increased incidence of swim bladder malformation, increased incidence of spinal curvature, and decreased heart rate. These results suggest that maternally deposited TBCO has similar effects on early life stage fish

development as does direct waterborne exposure. Effects of TBCO on reproduction in the F1 generation are currently being investigated and will be presented.

LEARNING AND HAND USE IN CRICKET PREDATION BY THE MOUSE

Liam Galvin, Behroo Mirzaagha | Supervisor: Ian Whishaw
(Department of Neuroscience, University of Lethbridge)

Although the mouse, Mus musculus, is preyed upon by many other species of animals, it is also a predator and will hunt and consume crickets. There has been no previous description of mouse predatory behaviour and no description of how mice learn to hunt, and this was the purpose of the present study. Mice given a single daily exposure to a cricket over 25-day study period displayed a number of phases in hunting: stalking, in which a mouse periodically encounter a cricket and often bit at it; pursuit, in which approach remained focused on the cricket until it was captured; and consumption, in which the cricket was decapitated, its core is eaten, and its shell discorded. Cricket capture and eating involved use of both the mouth and the hands. Over the duration of the study, the time to complete each behaviour became shorter with each cricket. The analysis suggests that stalking is analogous to Felid prey play, whereas pursuit and capture are analogous to Felid predation. That the hands are used for both cricket capture and cricket handing, suggests that predatory behaviour likely contributed to evolution of the skilled hand use of the mouse. Although visual and auditory cues may be used for cricket location, the vibrissae appeared to provide dominant guidance in pursuit and capture. This study highlights the complexity of mouse predatory behaviour, and the rapidity with which the behaviour is acquired. The study also highlights the complexity of hand mouth use and shows that the use of the hand in prey capture evolved well before its proposed evolution in the primate lineage.

A NOVEL PIPELINE FOR METHANOGEN COMMUNITY ANALYSIS VIA ILLUMINA DNA SEQUENCING DATA

Daniel Grant | Supervisor: Kristian Smits
(Department of Kinesiology, University of Lethbridge)

Interest in studying methanogens is increasing as researchers attempt to identify sources of greenhouse gases. Methanogens in forest ecosystems are increasingly being recognized as a significant source of methane, a potent greenhouse gas. This group of methane producing Archaea are obligate anaerobes and difficult to cultivate. The development of non-culture-based methods such as next generation sequencing (NGS) has provided an alternative, high throughput approach to studying the ecology of methanogens. However, analysis of NGS data requires a significant investment of time and effort into learning requisite skills in areas such as computer science and biostatistics. For this reason, accessible and practical approaches to analyzing this data are required. To address this issue, a user-friendly interactive pipeline for the analysis of NGS data was created using the existing DADA2 R package, providing exact and statistically supported DNA sequence analysis. In addition, an updated methanogen (mcrA) DNA reference database was compiled for use with this pipeline. The pipeline moves stepwise through parameter optimization and allows for iterative tuning of model parameters to ensure accuracy of results. Following sequence analysis and accurate taxonomic classification, publication quality figures will be created automatically for abundance, diversity and phylogenetic analyses. Results from this pipeline were identical to those obtained via manual analyses, with greater taxonomic classification using the updated methanogen database. This project addressed some shortcomings of analyzing NGS data by providing a simple approach for bioinformatic analysis of sequence data.

BIOL-16

INVESTIGATION OF A NOVEL "CLUMP" PHENOTYPE OBSERVED WITH STAPHYLOCOCCUS EPIDERMIDIS TREATED WITH PRAIRIE PLANT EXTRACTS

Nadia Hand, Leanne DuMontier | Supervisor: Sophie Kernéis
(Department of Biological Sciences, University of Lethbridge)

Antimicrobial resistance (AMR) decreases the effectiveness of antimicrobials, as pathogens can withstand their effects, making it harder to treat infections. Microbes, particularly ESKAPE pathogens (E. faecium, S. aureus, K. pneumoniae, A. baumannii, P. aeruginosa, and Enterobacter spp) are becoming resistant to currently available drug treatments; AMR has been identified as a global health issue. The Microbial Research Laboratory at the Lethbridge College is turning to prairie plants in southern Alberta in search of natural antimicrobial compounds. Several plant extracts have been found to cause a unique "clumped" phenotype in Staphylococcus epidermidis. The species can be found living alone, or in microbial communities known as biofilms and is a model for the ESKAPE pathogen, Staphylococcus aureus. This project's purpose is to characterize this phenotype and determine whether it is the result of plant extracts acting as an adherent between cells, a biofilm inducing compound, or both. This study has found that time to produce clumps is dependent on bacterial concentration. It has also been found that clumped bacteria are living, and that clumps contain >90% of cells in the sample. The most compelling observation is that when S. epidermidis is fixed (thereby killed) in glutaraldehyde, the clumped phenotype is still achieved in favour of a plant binding agent present in the extract. Because biofilms require a self-produced exopolysaccharide matrix, initial clumping is not the result of biofilm formation. This observation rules out the hypothesis that the plant extracts are only inducing biofilms. However, it is yet to be discerned whether clumped S. epidermidis are only adhered together or if clumping enables them to form a biofilm through density-dependent intercellular signaling. With this discovery, more information may be determined about this phenotype and its possible applications such as water filtration, and bacteria immobilization.

BIOL-18

AN ANALYSIS OF FORKED-LIKE GENE EXPRESSION IN THE VASCULAR CAMBIUM DURING INDUCED SECONDARY GROWTH

Melissa Hickle | Supervisor: Elizabeth Schultz
(Department of Biology, University of Lethbridge)

In the stem, secondary vascular tissue, including wood, arises from cellular divisions of the vascular cambium. Secondary growth requires the phytohormone auxin which is known to induce a number of genes which are expressed in the vascular tissues of plants. In this study, we investigated the expression of the FORKED1 (FKD1), FORKED-LIKE1 (FL1), and FORKED-LIKE2 (FL2) genes of the FORKED-LIKE (FL) gene family in the vascular cambium of Arabidopsis thaliana. These genes had previously been identified as part of the auxin response leading to vascularization in the leaves of Arabidopsis, however, their expression had yet to be investigated in the stem, which is the focus of this study. First, I modified a weighting method to induce secondary vascular tissue in the stems of Arabidopsis. Toluidine blue staining of hand sections revealed successful cambial induction and the formation of secondary tissue. Once the weighting method proved effective, I induced secondary growth in transgenic lines of Arabidopsis, with FL gene promoter fusions to the reporter gene GUS (FKD1:GUS, FL1:GUS, and FL2:GUS). During secondary growth of the vascular tissue, I visualized FL gene expression within stem sections via GUS staining methods and compared them to expression of the auxin reporter genes DR5:GUS and ATHB8:GUS. The preliminary results of this study have provided the first evidence of expression of FKD1 and FL1 in the vascular cambium with expression seen in dividing and newly formed cells. These findings suggest similarities between the vascularization mechanisms involving the FL genes in the leaves and stems of Arabidopsis and have potential applications in woody plants.

BIOL-19

TOXICITY OF BENZOTRIAZOLE ULTRAVIOLET STABILIZERS (UV-P, UV-9, UV-090) TO EARLY LIFE STAGE DEVELOPMENT OF ZEBRAFISH (DANIO RERIO)

Hunter Johnson, Jonathon Doering, Justin Dubiel | Supervisor: Steve Wiseman
(Department of Biological sciences, University of Lethbridge)

Plastic debris is a ubiquitous contaminant in environments globally. Plastics contain various chemical compounds that enhance the longevity and quality of the product. Specifically, the addition of benzotriazole ultraviolet stabilizers (BUVS's) helps prevent the degradation and discoloration of plastic materials. Due to improper disposal of plastics, chemicals such as BUVS's can leach and into aquatic ecosystems. As a result, BUVS's are ubiquitously detected in the aquatic environment and biota, causing concern for the health of fishes and other aquatic wildlife. There is currently only limited toxicity data present for BUVS's, but these studies suggest that certain BUVS's might dysregulate the aryl hydrocarbon receptor (AhR) causing early life stage toxicity in fishes. Therefore, there is need for a more comprehensive analysis of the effects caused by exposure to BUVS's and risks posed by these chemicals. The present study exposed embryos of zebrafish (Danio rerio) to precise serial doses of three priority BUVS's, namely2-(benzotriazol-2-yl)-4-methylphenol (UV-P), 2-(Benzotriazol-2-yl)-4-methyl-6-prop-2-enyl-phenol (UV-9), or 2-[3-(2H-benzotriazol-2-yl)-4-hydroxyphenyl]ethyl methacrylate (UV-090) through microinjection. Toxicity of each priority BUVS was assessed by recording early life stage malformations and mortality. Embryos exposed to BUVS experienced mortality in a dose-dependent manner, with UV-9, the most potent chemical tested, having a median lethal dose (LD50) of 6492 ng/g-egg and UV-090 being the least potent with an LD50 of 35209 ng/g-egg. Additionally, the extent to which each of the BUVS activates the AhR will be determined with a luciferase reporter gene (LRG) assay using COS-7 cells transfected with the AhR of zebrafish and three native fish species of regulatory concern in Canada. Results from this study will guide more objective assessment of risks posed by BUVS's for the protection of Canada's diverse populations of fishes.

BIOL-21

FEEDLOTS TO SEWAGE: METAGENOMICS IN A ONE HEALTH APPROACH TO ANTIMICROBIAL RESISTANCE

Catrione Lee, Rodrigo Ortega Polo, Rahat Zaheer, Brent Selinger | Supervisor: Tim McAllister
(Department of Biological Sciences, University of Lethbridge)

Antimicrobial resistance (AMR) is a rising concern in the One Health continuum. Concerns of the transmissibility of resistance genes from bacterial communities to another, between the three One Health continuum sectors – public health, environment, and agriculture which may act as reservoirs – have been raised. One method of tracking antimicrobial resistance through the environment is to use metagenomic sequencing of various agricultural and environmental microbiomes to search for antimicrobial resistance genes (ARGs) and characterizing their genomic contexts such as mobile genetic elements – like integrative conjugative elements (ICE) and plasmids. A dataset of 43 publicly available Illumina-sequenced shotgun metagenomic samples with 100-bp paired-end reads was selected from a previously published study. The number of samples per environment was as follows: 20 feedlot fecal composite, 13 catch basin downstream of feedlots, 4 manured agricultural soil samples, and 6 municipal sewage influent. Each sample's sequenced reads were taxonomically classified. For a focused analysis, a single fecal composite sample was selected to troubleshoot and optimize analysis. Targeted assemblies for analyzing ARGs' genomic context and searching for ICEs were accomplished through the tool MetaCherchant. De novo metagenomic assemblies were performed for all samples' reads to construct metagenomic-assembled genomes, and were then filtered based on quality, completeness, and contamination. These provided enough context to detect ARG-associated ICEs within the fecal sample. Further work will be done to establish an automated pipeline of the above analyses across all microbiome samples using the de novo assemblies.

IT-01

A UNIFIED VIEW OF EPIDEMIOLOGICAL AND ARTIFICIAL INTELLIGENCE BASED MODELLING TO APPLY EMPIRICAL EVIDENCES IN RATIONAL PUBLIC HEALTH POLICY MEASURES

Ali Boukrich | Supervisor: Baidya Nath Saha
(Department of Mathematical and Physical Sciences, Concordia University of Edmonton)

With the continued increase of COVID-19 variants of concern artificial intelligence based modelling could prevent the complete lockdown due to possible third wave of COVID-19 by adopting suitable public health measures. Policy making in these highly uncertain, complex, and rapidly changing environment have been extremely challenging. Epidemiological models (EPM) can be very helpful to understand the transmission dynamics of infectious diseases. However, the success of EPM depends on the optimal values of the parameters, which are typically adjusted manually by the domain expert through time-consuming, laborious, and burdensome trial and error procedures. In recent year, the availability of greater volumes and sources of data and advances in digital capabilities have empowered Machine Learning (ML) in predictive analytics including COVID-19 disease prediction. However, ML based black box models lack interpretability and explainability and therefore the paucity of transparency and accountability of ML based predictive models can have severe consequences in trust sensitive healthcare environments which urges evidence based rational policy making practices.

This study is unique of its kind which addresses the synergy between epidemiological and ML Based Modelling to leverage both genus of modelling techniques to bridge the gap between empirical evidence and public policy measures for infectious disease modelling: ML helps to estimate parameter of EPM; and EPM accelerates the convergence and increases the explainability of ML based predictive models and thus form a mutualism type symbiotic relationship. The proposed indelible model is inherently very generic in nature which could make significant contributions for other infectious disease modeling and improve preparedness and response for the future pandemic. This research envisages moving one step ahead, toward advances in fundamental computational tools development for epidemiological research.

IT-02

SAFE AI: PRIVACY PRESERVING MACHINE LEARNING ALGORITHMS FOR TRUST SENSITIVE ENVIRONMENTS

Jainth Chaudhary | Supervisor: Baidya Nath Saha
(Department of Mathematical and Physical Sciences, Concordia University of Edmonton)

Objectives: Despite the breakthrough success of Machine Learning (ML) algorithms - especially Deep Learning - in a broad spectrum of big data applications, cyberspace threats and vulnerabilities to ML systems raise major concerns in security- and trust- sensitive environments such as healthcare, defense, finance, government organization, and social network. A novel combination of ML techniques and privacy mechanisms is of the utmost importance for enabling secure privacy-preserving ML algorithms by making a trade-off between security and performance in ML systems.

Research Approaches: Homomorphic encryption (HE) allows computations over encrypted data and thus preserves privacy in a cloud computing environment. HE could be categorized into two main categories; partially homomorphic encryption (PHE), and fully homomorphic encryption (FHE). FHE can help solve privacy issues completely, but it introduces high performance overhead. To avoid such overhead, PHE can be used. In this research we evaluated the performance of different ML algorithms such as regression, neural network, and deep learning over both PHE and

FHE and an extensive comparative studies have been conducted in a broad range of privacy sensitive environments such as employee salary prediction, sentiment analysis from reviews data, email spam classification, handwritten digit recognition, and credit card screening.

Novelty and expected significance: This research provides a far insight on the trade-off between performance and security for a wide number of combinations of cryptographic and ML algorithms for constructing a secure PPDML system which have been tested on a number of trust sensitive applications. This research envisages moving one step towards bridging the knowledge gap between the ML and cryptography communities, which is the paramount requirement for addressing privacy concerns adequately in ML systems.

IT-04

COVID-19 CHATBOT: A NATURAL LANGUAGE PROCESSING AND ARTIFICIAL INTELLIGENCE POWERED INTELLIGENT VIRTUAL ASSISTANT TO CREATE AWARENESS DURING PANDEMIC

Shubham Malhotra | Supervisor: Baidya Nath Saha
(Department of Mathematical and Physical Sciences, Concordia University of Edmonton)

With the continued increase of COVID-19 variants of concern, ramping up the vaccination programs is not sufficient enough to prevent the rapid acceleration of the epidemic. Technology could prevent the complete lockdown due to possible third wave of COVID-19 by adopting suitable public health measures and individual precautions which is crucial to reducing infection rates and its severe outcomes, including hospitalization and deaths. The Machine Learning (ML) based digital assistant would facilitate rapid self-assessment of the individual using present physical symptoms, pre-existing medical condition, travel history, and neighbourhood corona map. Chatbot Graphical User Interface (GUI) has been developed by python tkinter. Natural Language Processing (NLP) helps provide context and meaning to text-based user inputs so that Artificial Intelligence (AI) can come up with the best response. Proposed chatbot offers advanced NLP capabilities which enables to identify spelling and grammatical errors and allow the chatbot to interpret intended messages despite the mistakes. NLP components of the COVID-19 chatbot include tokenization, lemmatization, and Bag-of-Words (BoW). This AI based digital assistant would not only be useful to respond COVID-19, it would build the infrastructures and processes to ensure that things flow more quickly and efficiently for other infectious diseases and in the wake of the next possible pandemic. Architectural design of the chatbot has been carefully developed to leverage its usability, reusability of components, flexibility, maintainability, and portability. The current version of the chatbot use keyword matching, and ML to retrieve the best answer or response from a pre-built question-answer bank. In future, we would like to enhance its computational capabilities which would enable to generate new dialogue based on the conversation training data using sophisticated AI based techniques such as deep reinforcement and adversarial learning.

IT-05

VIRTUAL COOK 2.0: A USER INTERACTIVE WEB BASED SMART RECIPE SEARCH ENGINE IN FLASK FRAMEWORK WITH JQUERY AND AJAX

Shubhampreet Singh | Supervisor: Baidya Nath Saha
(Department of Mathematical and Physical Sciences, Concordia University of Edmonton)

In this research we developed a web program called "The Virtual Cook" that can help people to get recipes of dishes, provided by limited ingredients. In addition, this program helps users to store their preferred dishes on their personal dashboard where they can post their reviews and images of dishes. Here we propose a formal model which allows us to effectively represent and search for recipes in online environments. The proposed model is an entity-relationship model that provides relevant entity types and properties, formalized as an ontology. The important aspects of the recipe model are identified by means of competency questions. Our model advances the state of the art in that it

supports essential queries that are typically not supported by websites and existing reference data models.

Virtual cook offers artificial intelligence powered digital intelligence supported by Web 2.0 which provides a full-featured Model-View-Controller framework under client-server architecture. This research extensively conducted software analysis and design processes including requirements specification, use-cases, system architecture, user interface prototype, and entity-relationship model. Technologies used to develop the system include python, MySQL, Flask, HTML, jQuery and Ajax. Flask framework enhances scalability, speed, system functionality, maintainability, security, and portability.

Virtual Cook offers a user interactive web 2.0 based smart recipe search engine which help users to find dishes from limited ingredients. We exploit a ranking algorithm to sort the dishes based on users rating. A comprehensive list of tasks to develop the Virtual Cook web 2.0 based recipe search engine includes Web engineering, Web design, Web content development, client-side/server-side scripting, Web server, network security configuration, and e - commerce services. We illustrate the methodology followed, the developed model, and the evaluation we conducted.

IT-03
APPLICATION OF AN SVEIRD MODEL TO TRACK THE SPREAD OF COVID-19 IN NIGERIA

Angela Li, Crystal Wai, Timothy Puffer | Supervisor: Ashok Krishnamurthy
(Department of Math and Computing, Mount Royal University)

Background: The Nigeria Center for Disease Control (NCDC) is reporting a steady increase in the number of confirmed COVID-19 cases. Reliable information regarding the nature of the spread is imperative for Nigerian policy makers and citizens to make educated decisions on safety measures moving forward.

Rationale: It is essential to understand what future epidemic trends will be, as well as the effectiveness and potential impact of government disease intervention measures.

Methods: We present a spatial SVEIRD (which stands for Susceptible, Vaccinated, Exposed, Infectious, Recovered and Dead compartments) epidemic model to capture the transmission dynamics of the spread COVID-19 and provide insight that would support the NCDC towards informed, data-driven decision making. Using the 2020 population count data from WorldPop as a gridded raster map we assess the geographical spread COVID-19. Each grid cell has a population count, which is divided into disease compartments. Each grid cell can transmit disease to its neighbors, with probabilities that decline exponentially with the Euclidean distance.

Results: We use the spatial epidemic model to estimate and project the number of newly infected and death cases up to August 1, 2021. We present spatio-temporal disease maps for the infectious variable for the progress of COVID-19 in Nigeria.

Conclusions: Predicting the transmission dynamics of COVID-19 in Nigeria is challenging and comes with a lot of uncertainty. First, we run the spatial simulations under the worst-case scenario, in which there are no major public health interventions. Next, we account for mitigation efforts including strict mask wearing and social distancing mandates, targeted lockdowns, and widespread vaccine rollout to vaccinate priority groups. Predictions for disease prevalence with and without mitigation efforts are presented via time-series graphs for the epidemic compartments.

SESSION B5 | 9:15 AM - 12:00 PM

HS-08

IMPACT OF CD36 MUTANT ON FATTY ACID UPTAKE

Ramesh Mahdavifar | Supervisor: Maria Febbraio
(Department of Psychology, University of Alberta)

Fats are a component of our diet and are essential to human survival, however, excess amounts can lead to diabetes, stroke, obesity and numerous cardiovascular diseases. Long chain fatty acids (LCFA) possess over 12 carbons, entering the cell by two means: flip-flop passive diffusion and a protein-mediated mechanism in which LCFA requires the help of a specific protein. A significant protein correlated with LCFA uptake is cluster of differentiation 36 (CD36). Lysine at residue 164 of the CD36 protein is associated with fatty acid uptake, thus, a single point mutation, K164Q, will be examined for its impact on LCFA uptake. Furthermore, to rule out that CD36 signalling may be influencing LCFA uptake, we will determine if the K164Q mutation disrupts the signalling. Wildtype and K164Q mutants of CD36 were engineered with a GFPSpark tag previously. Initially, HEK-Blue cells were transfected and underwent immunofluorescence analysis to assess expression. In addition, HEK-Blue cells express Toll-like Receptor 2 (TLR2) and a nuclear factor kappa B (NF-κB) reporter gene. Because CD36 cooperates with TLR2, changes in Secreted Alkaline Phosphatase (SEAP) expression are a measure of CD36 signalling. Following transfection, a SEAP Assay was performed, and we observed similar SEAP expressions in Wildtype and K164Q. Due to the similar expressions, we deduced that K164Q mutation did not disrupt CD36 signalling. Despite promising results, lack of time did not allow for further experiments. Future experiments should include a BODIPY Fatty Acid Uptake Assay in order to test whether the K164Q mutation decreases fatty acid uptake.

HS-09

ASSEMBLING AN ATOMIC MODEL OF THE HIV-1 VIRAL SPIKE ENVELOPE GLYCOPROTEIN: IMPLICATIONS FOR VIRAL ENTRY

Tarana (Riya) Mangukia, Joy Ramielle L. Santos, Weijie Sun, Eduardo Reyes-Serratos | Supervisor: Marcelo Marcet
(Department of Medicine, University of Alberta)

Despite the discovery of type 1 human immunodeficiency virus (HIV-1) in the early 1980s, significant knowledge gaps remain in our understanding of the structure of viral spike envelope (Env) glycoproteins. These proteins originate from a larger glycoprotein-160 (gp160) precursor and are later cleaved by intracellular proteases to generate gp41 and gp120 trimers, which are eventually incorporated into a mature HIV-1 particle. The Env protein has a crucial role in interacting with the matrix shell (MA) of the HIV-1 particle and facilitating viral entry by interacting with receptors and coreceptors located on T-cells. Current models only assess portions of the Env protein; there is, therefore, no fully resolved structure of the HIV-1 Env glycoprotein. Developing a complete, accurate model of the Env protein at the atomic level was necessary to better understand the mechanism of viral entry. In this abstract, we assemble the Env protein entirely as an all-atom simulation model using a combination of predetermined Env protein domains from X-ray crystallography, nuclear magnetic resonance (NMR), cryo-electron tomography and three-dimensional prediction tools. The overall structure was determined to be 19.27 nm in height and the cytosolic (CT) domain 5.64 nm wide. The determination of the structure allows future models to take into account the distance, orientation and interaction of Env proteins with the various structural components of HIV-1 to determine the HIV-1 mechanism of viral entry.

HS-13

ASSESSMENT OF ADHERENCE TO PERIOPERATIVE ANTICOAGULATION DISCONTINUATION GUIDELINES IN PATIENTS WITH ATRIAL FIBRILLATION AND PREVIOUS STROKE

Mujtaba Siddique, Asif Butt and Nazeem Arsalan | Supervisor: Ashfaq Shuaib
(Department of Neurology, University of Alberta)

Introduction: A quarter of all the strokes are caused by atrial fibrillation (AF). Anticoagulants (ACT) work by preventing the formation of blood clots and are given to patients with AF to prevent stroke. Annually, 15% of patients who receive oral anticoagulation require interruption for surgery or an invasive procedure. This study evaluates the adherence of patients with AF and previous stroke to the Canadian perioperative guidelines for the discontinuation and reinitiating of anticoagulation.

Methods: Data was collected from a prospective patient survey at the stroke prevention clinic University of Alberta hospital. Patients charts were reviewed from the AHS database and adherence was looked at according to the Thrombosis Canada Perioperative guidelines for the discontinuation of anticoagulants.

Results: During the study period (2016-2019), there were 509 patient charts reviewed. Anticoagulation treatment was interrupted in 150 patients. Out of the 150 patients who discontinued their ACT, 98 discontinued for surgical or invasive procedures. The interruption was adherent to guidelines in 29 (29.6%) of patients and inappropriate or non adherent in 69 (70.4%) patients. Patients who inappropriately discontinued were split into two groups, one group that discontinued for longer than guideline recommended 61 (62.2%) and patients whose ACT discontinuation was shorter than guidelines recommended 8 (8.2%). There were 7 ischemic strokes recorded during the ACT discontinuation. The strokes were significantly more in patients where ACT treatment was delayed (6/61 or 9.8%) compared to appropriate re-anticoagulation (1/29 or 3.4%). There were no strokes or hemorrhages in patients where ACT was initiated earlier than recommended.

Conclusion: Our results indicate a great discrepancy between the recommended perioperative anticoagulation guidelines and the actual practice of these guidelines. Delay in re-anticoagulation results in significantly higher embolic complications.

HS-14

ANTI-VEGF SWITCH THERAPY IN RADIATION RETINOPATHY

Ojas Srivastava | Supervisor: Ezekiel Weis
(MD Program, University of Alberta)

Purpose: Uveal melanoma is the most common ocular malignancy. Enucleation was the traditional treatment until the introduction of radiotherapy. Radiation retinopathy is a dose-dependent complication of the retina following exposure to radiation. Radiation retinopathy is managed by anti-vascular endothelial growth factors (anti-VEGF) agents. Monthly administration of the anti-VEGF agent bevacizumab is the traditional treatment for radiation retinopathy. The objective of this study is to assess patients' response to aflibercept, a new anti-VEGF agent, in those who have failed treatment by bevacizumab. It is hypothesized that a portion of patients who failed anti-VEGF agent bevacizumab will respond to aflibercept.

Methods: A prospective case-series of patients with clinically significant radiation maculopathy were enrolled. Standardized testing, as part of the Alberta Ocular Brachytherapy program, was performed on all patients in Calgary and Edmonton. Visual and retinal response to therapy was assessed with regression analyses.

Results: Thirty patients, 17 female and 13 male, with a mean age of 57 years (±15) underwent the switch from monthly

bevacizumab treatment to aflibercept. Regression analysis showed statistically significant differences between bevacizumab and treatment by aflibercept at one month (P=0.003, P=0.02), three months (P=0.004, P=0.004), and six months (P=0.003, P=0.013) in both retinal thickness and visual acuity, respectively.

Conclusions: This study highlights that if the traditional anti-VEGF agent is not successful, patients can show clinical improvements from a switch to aflibercept. Future studies will benefit from a larger series in to quantify this response in a multicentre trial and larger patient cohort.

OTHER-03
CONTRIBUTIONS OF EXECUTIVE FUNCTION TO PARENTING

Jenny Le, Larissa Predy | Supervisor: Sandra Wiebe
(Department of Psychology, University of Alberta)

Executive function (EF) skills may be important in effective parenting. Research has shown that negative parenting practices have been found to be related to EF task performance deficits across several domains, namely working memory, inhibitory control, attention/set shifting, and planning. The role of parenting attitudes and attributions also plays a critical role in understanding the link between executive function and parenting, such that the ability to accurately perceive a child's intentions affects parental responses to undesirable behaviour. Furthermore, the relationship between EF and parenting measures may be moderated by factors that affect EF such as stress. EFs are cognitive functions necessary for cognitive control. They are skills essential not just for cognitive health, but social, emotional, and physical health. Considering the risk of impaired or lowered EF performance during the early years of parenting, it is important to understand the ways in which EFs are related to parenting. To date, there is limited research on the association between parenting and executive function, and particularly variables that may be moderating this relationship. This study's objectives are to: a) examine whether there is a positive association between executive function and parenting measures and b) examine whether there are any moderating variables within the association between executive function and parenting measures. I hypothesize that there is a link between executive function and parenting measures, such that poorer executive function predicts negative parenting, and higher executive function predicts positive parenting practices. Preliminary data analyses are ongoing, using questionnaires assessing parenting and EF tasks.

OTHER-06
AGAINST THE GRAIN: PROMOTING IDENTITY CONTINUITY AS A STRATEGY TO ELEVATE GROUP SUPPORT FOR CHANGE

Emma Monaghan, Lily Syfers | Supervisor: David Rast
(Department of Psychology, University of Alberta)

Change is often resisted, despite being essential for social and organizational progress. Change resistance can be rooted in threats to group identity continuity, which is the perception that the core characteristics of the group remain stable over time (Smeekes & Verkuyten, 2015). Although prototypical leaders can effectively reduce change opposition by promoting continuity (van Knippenberg, van Knippenberg, & Bobbio, 2008), change produces uncertainty that increases support for non-prototypical leaders. This study investigated how identity continuity, leader prototypicality, and uncertainty impact support for anti-normative change. An online between subjects experiment (N = 189) manipulated leader prototypicality (prototypical or non-prototypical), identity continuity rhetoric (continuity or discontinuity) and uncertainty (high or low). Participants indicated their support for an unpopular change initiative, removing campus beer gardens. There was no significant interaction between identity continuity rhetoric, leader prototypicality and uncertainty. Future studies could correct methodology limitations, such as a change initiative that is too peripheral to the group identity to incite discontinuity threats. Further investigation of UA student values could be integrated into the change message. Participants in our study were apathetic towards the change message; therefore, determining a group's central values is critical to producing statistically significant results. Future researchers can

reduce apathy by describing how the change message impacts collective self definition. These results contribute to a valuable research direction by outlining how to refine identity continuity methodology. Using rhetoric emphasizing identity continuity may be an effective tactic to reduce opposition to anti-normative change by promoting a stable sense of identity and direction.

HS-15

INOCULUM EFFECTS IN STAPHYLOCOCCUS AUREUS ISOLATED FROM THE AIRWAYS OF INDIVIDUALS WITH CYSTIC FIBROSIS

Julianna Svishchuk | Supervisor: Michael Parkins
(Department of Cellular, Molecular and Microbial Biology, University of Calgary)

Staphylococcus aureus (S. aureus) is one of the most important human pathogens in the context of infectious disease. Understanding factors that influence its response to antibiotics and resulting patient outcomes is integral if improvements are to be realized.

In particular, methicillin-sensitive S. aureus (MSSA) is responsible for 80% of S. aureus-related diseases in Canada. Recent literature has confirmed that many strains of MSSA possess resistance to certain β-lactam antibiotics, such as cefazolin, but only when tested at higher concentrations than those used in clinical laboratories ($\geq 10^5$ µg/mL). This effect, termed the high inoculum effect (HIE), is not detected in current testing parameters. However, multiple studies have demonstrated that patients with MSSA blood-stream infections with HIE have worse outcomes when treated.

Cystic fibrosis (CF) is a complex multi-system disease most notable for respiratory pathology. MSSA is the most common pathogen infecting individuals with CF – and optimizing treatments of MSSA-related lung infections is necessary to improve CF-related outcomes. Due to the fact that MSSA infecting CF airways may reach concentrations as high as 10^8 CFU/mL, understanding the prevalence of this phenomenon and its impact is key.

My project focuses on screening a set of approximately 300-CF derived MSSA isolates (yearly isolates from 2016-2018 from all attendees of the Calgary Adult CF Clinic) for the HIE in cefazolin and other clinically relevant antibiotics. Factors associated with risk of HIE, including underling blaZ gene type are currently being investigated.

HS-18

WHAT NUTRITIONAL INTERVENTIONS EXIST FOR CANADIAN INDIGENOUS ADULTS? A SCOPING REVIEW

Jessica Zhang, Levi Frehich | Supervisor: Sonja Wicklum
(Department of Family Medicine, University of Calgary)

Colonization and racism imposed through Canadian policy have harmed the family structure and led to intergenerational trauma within Indigenous communities. This unique consequence to Indigenous social determinants of health in combination with nutritional insecurity compromise well-being. Nutritional insecurity, due to rising prices, climate change and the nutrition transition, coupled with a lack of access to physical activity resources also contribute to rates of obesity and associated diabetes and cardiovascular diseases observed in Indigenous populations. We sought to explore the scope of published literature on nutritional interventions for Indigenous adults in Canada.

Methods: We conducted a scoping review on Indigenous nutrition interventions in Canada based on the Arksey and O'Malley framework. The search included eight databases and grey literature to identify relevant studies. Using Covidence® software, a research assistant and two researchers executed screening and data extraction. The extraction was performed using a designed extraction template.

Results: The scoping review identified 11918 unique studies published before July 2020. After abstract/title screening,

283 remained. 22 were included for final data extraction. No additional studies were identified in the grey literature. Identified interventions were grouped by geography, intervention type, and limitations. Key themes revealed were Northern Canadian Communities Focus, Country Food, Multifactorial (ie., additional health components to nutrition) and Clinical (i.e., prenatal and diabetes focus). Majority were at the community level with two at the individual.

Discussion/Conclusions: These findings will inform current and future health research programming regarding Canadian Indigenous populations. Specifically, it will inform the Wolf Trail Program, a holistic wellness program for Indigenous women, ensuring incorporation of identified best nutritional practices.

HS-07

THE EFFECTS OF PRECONCEPTION MATERNAL NICOTINE AND ALCOHOL ON ADULT OFFSPRING HIPPOCAMPAL VOLUME AND ASSOCIATED BEHAVIOR

Kennedy Lewis, Robbin Gibb, Allonna Harker | Supervisor: Serena Jenkins
(Department of Neuroscience, University of Lethbridge)

This study examined the influence of chronic preconception maternal nicotine and alcohol on hippocampal volume and behavior of adult offspring. In the nicotine experiment, female Long-Evans rats were randomly assigned to paired- or enriched-housing, received nicotine (15mg/L in 1% sucralose) or sucralose (1%) in their drinking water for 7 weeks, then were mated with naïve males. The alcohol experiment replicated these methods without the housing treatment; ethanol (up to 20%) was added to the drinking water of the treated females, and the control females received plain water. Offspring were tested in the Elevated Plus Maze (EPM) and Morris Water Maze (MWM) as adults. These tests assess anxiety-like behavior that is associated with the ventral hippocampus (VH) and learning/memory/spatial navigation behaviors that are associated with the dorsal hippocampus (DH), respectively. Golgi-Cox-stained brains of the offspring were used to measure DH and VH volumes.

The nicotine experiment found that in the EPM, offspring from pair-housed dams exhibited higher anxiety-like behavior than those from enriched dams. In MWM, males located the hidden platform faster and with less distance than females. Sucralose offspring had a Drug x Housing interaction for MWM training latency, with those from enriched dams locating the platform faster. For the MWM probe, females traveled further than males. Males had greater DH volume than females. In the alcohol experiment, alcohol female offspring traveled a shorter distance than control females during MWM training; for the MWM probe, males traveled a further distance than females. There were no effects of alcohol in the EPM or on hippocampal volume.

These findings indicate that preconception maternal nicotine and alcohol consumption have long-term consequences on next-generation offspring. Therefore, those of child-bearing age should be made aware of the possible influence of preconception drug use on the brain and behavior of future offspring.

SESSION B6 | 9:15 AM - 12:00 PM

MATH-04

THE PHYSICAL NATURE OF THE ONE-DIMENSIONAL CUBIC NONLINEAR SCHRÖDINGER EQUATION

Ana Mucalica | Supervisor: Ion Bica
(Department of Mathematics and Statistics, MacEwan University)

In his quest to explain a quantum particle's probabilistic nature, Erwin Schrödinger, in 1926, proposed a nonrelativistic wave equation, that would only require one initial condition, i.e., the initial displacement of an electron. His equation describes the wave-particle duality discovered by Louis de Broglie in 1924. Since in Schrödinger's equation, only the particle's position is well defined, the momentum satisfies the Uncertainty Principle, i.e., the particle can start moving in any direction. Schrödinger's wave equation is dimensionless, and this allows the equation to be a mathematical model describing different physical phenomena, particularly the soliton. A soliton displays a perfect balance between dispersion and nonlinearity, so a nonlinear term needs to accompany Schrödinger's initial equation. This presentation will explain the mathematics behind the two different physics in the one-dimensional cubic nonlinear Schrödinger's equation. The presentation will also include the demonstration of a novel theorem describing the steepening of the wavefront due to nonlinearity.

MATH-02

USING THE LLL-ALGORITHM TO BREAK THE RSA CRYPTOSYSTEM

Khoa Bui | Supervisor: Dr Ha Tran
(Department of Mathematics and Physical Sciences, Concordia University of Edmonton)

The Rivest-Shamir-Adleman (RSA) cryptosystem is one of the most popular cryptosystems being used in secure data transmission. Until today, the cryptosystem is still considered to be safe due to the hardness of the factorization problem. The Lenstra-Lenstra-Lovász (LLL) algorithm offers various methods to attack the RSA cryptosystem, even going as far as potentially breaking the system by solving the factorization problem. In this presentation, we will discuss how a weak parameter creates deadly vulnerabilities in the RSA cryptosystem, and the usage of LLL-algorithm in the factorization problem.

MATH-03

IN ALL DIRECTIONS: HIGHER DIMENSIONAL ARITHMETIC PROGRESSIONS IN MEYER SETS

Anna Klick | Supervisor: Nicolae Strungaru
(Department of Mathematics and Statistics, MacEwan University)

We establish the existence of higher-dimensional arithmetic progressions of arbitrary length in Meyer sets, which gives a novel characterisation of fully Euclidean Meyer sets.

MATH-01

USING THE LLL ALGORITHM IN ATTACKING KNAPSACK CRYPTOSYSTEMS

Ali Boukrich | Supervisor: Dr Ha Tran
(Department of Mathematics, Concordia University of Edmonton)

Knapsack problems are relevant in the fields of complexity theory, applied mathematics and cryptography. In this project, we analyze the security of the knapsack cryptosystem using superincreasing sequences which is proposed by Merkle and Hellman. We will show that using the LLL algorithm one can break this public key system in polynomial time.

OTHER-01

MESSENGERS FROM THE ASTEROID BELT: A STUDY OF DIOGENITES NORTHWEST AFRICA 10268 AND 7464

Jannah Aizon | Supervisor: Erin Walton
(Department of Physical Science, MacEwan University)

The study of meteorites is crucial to understanding the geological evolution of our early solar system. In this study, we observe optical and chemical properties of two diogenite meteorites (Northwest Africa 7464 and 10268) that originated from the second-largest asteroid, 4 Vesta. By studying the mechanical deformation and transformation features of feldspar, olivine and pyroxene grains within the samples, we are able to constrain the shock stage of each meteorite. Northwest Africa 7464 and 10268 were both observed using a scanning electron microscope, an energy dispersive x-ray spectrometer, an electron microprobe, a petrographic microscope and a Raman spectrometer. Northwest Africa 7464 exhibits weak mosaicism and planar fractures in pyroxene, as well as, undulatory extinction and planar fractures in olivine. These features suggest a moderately-shocked S4 meteorite consistent with a shock pressure of between 4-20 GPa. Northwest Africa 10268 contains opaque shock veins associated with the diaplectic plagioclase glass, maskelynite. This host rock exhibits strong mosaicism and undulatory extinction in pyroxene, as well as, twinning in crystalline feldspar. These features are consistent with a strongly shocked S5 meteorite, experiencing a shock pressure of between 22-25 GPa. These results give insight on shock pressure and temperature conditions that occur on 4 Vesta.

PHYS-02

USING THREE-STATE ISING MODEL TO STUDY CANCER CELL RESPONSE TO CHEMOTHERAPEUTIC DRUGS

Ashley Hickey, Dylan Miller | Supervisors: Vahid Rezania, Dr Jack Tuszynski (University of Alberta)
(Department of Physical Sciences, MacEwan University)

Chemotherapeutic agents are assessed for their efficacies primarily by their ability to cause apoptosis of cancer cells and their potency is given by an IC50 value, the half of maximal inhibitory concentration. To treat cancer, both target-specific and systemic-action drugs and drug combinations have been used. As a result, it is necessary to correctly choose a drug type, its dosage and schedule for optimized drug selection and administration to reduce unwanted side effects. Therefore, a precise mathematical modeling to assess cancer cells' response to chemotherapeutic agents will be a great asset in the selection and/or scheduling process.

Recently, we adopted the spin-1/2 Ising model methodology and applied it to a series of cytotoxic drugs administered against numerous cancer cell lines in a dose–response manner. Here, we aim to generalize our approach and implement the spin-1 Ising model of phase transitions as an elegant and powerful mathematical approach to study cancer cells exposed to cytotoxic chemotherapeutic agents. The three-state model will provide a more accurate and consistent analysis of cytotoxic agents' effects on cancer cell lines and reveal the presence or absence of the bystander effect through the interaction constant.

OTHER-13

NUCLEAR ENERGY FROM DIFFERENT PERSPECTIVES

Luisa Vargas Suarez, Ronald Zachary Sumners | Supervisor: Jason M. Donev
(Department of Physics, University of Calgary)

For the past several years, the Energy Education project has been getting thousands of daily visits by people curious about energy. Part of the power of this site is the interactive data visualizations. Three simulations were built to help the public understand how nuclear science and technology can meet society's energy demands. The first two use publicly available data to illustrate the role of nuclear power in the energy stories of different countries, such as how it compares in terms of the production, imports, and exports of a given country. The following perspectives also help give the energy story of nuclear power: Total Primary Energy supply (TPES), Total Final Consumption (TFC), and conversion losses from turning TPES to TFC. The third simulation demystifies the nucleus' inner workings by linking the periodic table with the chart of the nuclides. These tools can foster enthusiasm about nuclear science and technology.

PHYS-01

ERROR CORRECTION IN QUANTUM KEY DISTRIBUTION (QKD) USING LOW DENSITY PARITY CHECK (LDPC) CODES

Snehasis Addy | Supervisor: Daniel Oblak
(Department of Physics and Astronomy, University of Calgary)

More than ever, our society relies on secure exchange of data and the ability to have confidential communication between people in different locations. However, advancements in both classical computation and research in quantum computing threaten the security of the classical encryption protocols that are currently used. Fortunately, quantum key distribution (QKD) provides an alternative method for data encryption, which is based on the principles of physics rather than assumptions of the computational power of the adversary. QKD is based on the transmission of bits encoded in quantum systems (qubits), such as single photons. In the simplest case of two parties seeking to establish a shared secret random bit-string (i.e. a secure encryption key), these qubits are encoded by one of the parties with randomly selected qubit values in a random basis before being sent over a public channel to the receiving party. The receiving party measures the qubit states in a random basis and a raw-key is generated. The raw-key contains errors due to imperfections and potential eavesdroppers. Hence, error-correction must be performed using a classical error-correction algorithm. The challenge is to design an algorithm that not only corrects all the errors efficiently but also leaks the least amount of information when used. The error-corrected sequence still cannot be considered as a secure-key because the information in the key might have been leaked by the attack of the eavesdropper. Therefore, the next step is privacy-amplification in which the privacy of the error corrected key is enhanced using universal hash functions and a final secure-key is generated. The project tackles the error correction part which is the most important part of the post-processing and is very essential for commercialization and real world application of QKD.

PHYS-03

THE 3D MORPHOLOGY OF MOLECULAR CLOUDS

Joshua Peltonen | Supervisor: Rene Plume
(Department of Physics and Astronomy, University of Calgary)

Mapping a diffuse object in space is a difficult task. Molecular clouds are unique in that they form stars within them. Therefore, if the location of young stellar objects (YSOs) within the cloud is known, this can indicate the cloud's structure. The significant difficulty is locating the positions of YSOs in the sky. Several molecular clouds have databases of known YSOs that include the position in the sky. We were able to correlate the positions of known

YSOs with Gaia data, which measures distance, to find the 3Dimensional position to several clouds' YSOs. Thus, the 3Dimensional structure of the clouds is now known. We also created a method of finding YSOs using all-sky infrared surveys. These all-sky surveys record colour data on every star in their catalogues. YSOs were identified using their unique colour properties. Once the YSOs are identified, 3Dimensional maps can be created for clouds that do not have databases of known YSOs.

SESSION C1 | 1:30 PM - 4:30 PM

BIOL-24

CHANGES IN THE ELEVATIONAL DISTRIBUTIONS OF PLANT SPECIES IN WATERTON LAKES NATIONAL PARK OVER 25 YEARS OF CLIMATE WARMING

Kirsty McFadyen, Jed Lloren | Supervisor: Jenny McCune
(Department of Biological Sciences, University of Lethbridge)

Climate change has the capacity to hugely alter plant distributions. Numerous plant species have been reported to exhibit upward elevational shifts in response to climate change, although this varies greatly among species and respective regions. Further, it is often difficult to isolate climate-driven effects on plant distributions at a local scale from other modes of disturbance. In this study, the effects of climate change on plant communities are evaluated in Waterton Lakes National Park using legacy study data from 101 vegetation plots surveyed in 1992 and resurveyed in 2019. The change over 25 years in the mean elevation of species distributions and the abundance-weighted mean elevation of species distributions is assessed. In addition, the association of 493 plant species with temperature is determined. The abundance weighted temperature affinity of plant communities is then evaluated.

BIOL-25

THE BRAIN AND CANNABIS: INVESTIGATING THE EFFECTS OF HIGH-CBD CANNABIS STRAINS ON MOTOR RECOVERY FOLLOWING STROKE

Jhanvi Mehta | Supervisor: Robbin Gibb
(Department of Neuroscience, University of Lethbridge)

The recent legalization and increasing accessibility of cannabis necessitates a more in-depth knowledge of this substance and both the short and long-term effects it has on behaviour. This growing industry has resulted in an emergence of novel cannabis strains, each with their own unique concentrations of cannabinoids such as tetrahydrocannabinol (THC) and cannabidiol (CBD). While THC is sought after for its psychedelic effects, CBD does not share these apparent psychoactive effects and has been found to possess anti-inflammatory and analgesic properties. These qualities are what makes it a molecule of particular interest when it comes to attenuating neurological damage on a cellular-scale—such as in stroke. Strokes are the third leading cause of death in Canada, and with the number of people in Canada of a vulnerable age increasing, the number of people living with the effects of having suffered a stroke can be expected to increase in the coming years. By mediating the cellular cascades that occur following stroke, it may be possible to minimize the cognitive and physical impairments patients face. CBD administration either prior to or post-stroke may allow for an accelerated recovery period, improved quality of life, and preservation of motor function. This study aims to assess whether high-CBD cannabis can be used to improve stroke outcomes via a rodent model. We will first utilize a behavioural test battery, neuroanatomical analysis, and western blotting to analyze the behavioural and physiological changes that result from cannabis consumption. We hypothesize that due to CBD's anti-inflammatory properties, there will be significant improvement in motor recovery between the extract-treated animals compared to controls with no negative side effect on the brain or on the animal's behaviour. The ultimate goal of this project is to open the door to providing a more natural, cost-effective, and easily accessible treatment for those affected by stroke.

BIOL-30

DETERMINING THE EFFECTS OF UV-STABILIZERS, UV-9 AND UV-090, ON OOCYTE MATURATION IN ZEBRAFISH (DANIO RERIO)

Yamin Raza, Justin Miller, Jon Doering | Supervisor: Steve Wiseman
(Department of Biological Sciences, University of Lethbridge)

Benzotriazole UV-Stabilizers (BUVs) are chemicals that protect against UV degradation. BUVs are found in industrial and consumer products and can enter aquatic environments via wastewater. Although studies have shown widespread contamination of BUVs, little is known about the toxicological effects. This study explored whether the BUVs, UV-9 and UV-090, impair reproduction of zebrafish (Danio rerio) by inhibition of oocyte maturation. Results were compared between oocyte maturation assays, where oocytes were exposed to BUVs in vitro or in vivo. To assess effects of in vitro exposure, stage IV oocytes were excised from sexually mature female zebrafish and exposed to various concentrations of each BUV, followed by a maturation-inducing hormone. When exposed to UV-9 in vitro, there was significantly less maturation between the control and the 200µg/L concentration of exposed oocytes. In the UV-090 exposure, there was significantly less maturation of oocytes exposed to 200, 2000, 20000µg/L concentrations, compared to the control. To assess effects of in vivo exposure, sexually mature female zebrafish were fed a diet of 25 (low), 125 (medium) or 625 (high) ng BUV/g food. Following 10-day exposure, stage IV oocytes were excised to assess maturation in response to maturation-inducing hormone. There was significantly less maturation of oocytes from fish exposed to UV-9 at 125 and 625ng/g food. However, there was no inhibition of oocytes from fish exposed to either concentration of UV-090. Overall, results suggest that UV-9 impairs oocyte maturation in vitro and in vivo; whereas UV-090 may be a less potent inhibitor of oocyte maturation because inhibition was only observed in vitro. Further studies are required to assess the effects of UV stabilizers on reproductive capacity and to determine whether assays of oocyte maturation are predictive of reproductive performance. This study increases understanding of possible toxicological effects of BUV exposure in aquatic wildlife.

BIOL-31

GERMINATION TRIALS AND PHENOLOGICAL ANALYSIS OF CANADA'S ENDANGERED WOOD POPPY (STYLOPHORUM DIPHYLLUM)

Jaxon Reiter | Supervisor: Jenny McCune
(Department of Biological Sciences, University of Lethbridge)

The wood poppy (Stylophorum diphyllum) is a herbaceous woodland plant listed as endangered under the Endangered Species Act of Ontario and Canada's Species at Risk Act. Plant translocation, or the intentional movement and establishment of a plant species, is listed in the recovery strategy for the wood poppy in Canada. Studies on ex-situ propagation and germination of the wood poppy are necessary for the development of a successful translocation project. We collected, stratified, and sowed seeds from two of the five known native Canadian populations and four commercial native plant nurseries and grew them in a common garden setting to determine if phenological differences exist between plants of Canadian and US origin. We hypothesized that differences in germination, growth, and development could be contributing to the rarity of S. diphyllum in Canada and may indicate genetic differences in these populations which are isolated from other populations within the species' North American range. We successfully germinated seeds from both native Canadian populations and three of four commercial native plant nurseries, achieving a germination rate of 51% for seed from Canadian populations, 34% for nursery seeds, and a total rate of 39% across all seed sources. We found differences between the germination rates, days from germination to first leaf emergence, and days to germination from sowing for each source. Plants from Canadian populations have a faster growth rate, a greater number of leaves, differences in leaf shape, and fewer trichomes than nursery plants of US origin. These results indicate that the wood poppy can be propagated successfully from Canadian seed sources and that Canadian wood poppy populations are likely genetically distinct from cultivated nursery stock. Our findings will inform the development of a translocation strategy in the future and set the stage for genetic analysis of these populations.

BIOL-38

MORPHOLOGICAL AND MOLECULAR IDENTIFICATION OF AIRBORNE FUNGAL SPORES IN POTATO FIELDS OF ALBERTA

Melissa Telfer | Supervisor: Dmytro Yevtushenko
(Department of Biology, University of Lethbridge)

Potato (Solanum tuberosum) crops in southern Alberta represent a significant proportion of agriculture covering 40,000 acres and generating over 128,000 lbs of product annually. However, disease incidence remains a major limiting factor in profitable potato production. Some of them, such as potato late blight caused by the oomycete pathogen Phytophthora infestans can spread by airborne spores and destroy an entire potato field in less than a week. Working with industry partners, we have established an early detection and diagnostics system to help potato growers improve disease management decisions and reduce the unnecessary pesticide applications in the absence of imminent pathogen pressure. The system utilizes a network of Burkard automatic multi-vial spore samplers, placed throughout potato growing regions in Alberta and used to monitor daily changes in airborne spore concentrations. The collected spores are examined under the microscope to identify morphological features that are characteristic to P. infestans, and well as the early blight pathogen Alternaria solani and Fusarium species, and their numbers reported to the growers. The aim of this study was to develop a molecular diagnostics protocol to confirm species identity of spores that resembled morphology of P. infestans but were inconclusive under light microscopy. The individual spores were germinated on KV-8 medium in vitro, followed by isolation of pure cultures. DNA was extracted from actively growing mycelium and amplified using conventional PCR and two pairs of universal primers targeting 28S rDNA and ITS regions. The amplified DNA fragments were ligated into plasmid DNA, cloned into E. coli cells, and analyzed by DNA sequencing. The results confirmed species as F. avenaceum, F. equiseti and Parastagonospora nodorum. The developed molecular detection technology improves the accuracy of disease risk prediction and has the potential to reduce the use of fungicides in the environment.

SESSION C2 | 1:30 PM - 4:30 PM

ENVSCI-01

DETERMINATION OF BASELINE SOIL ORGANIC MATTER AND 13C STABLE ISOTOPE PRIOR TO BIOSOLIDS APPLICATION.

Els Hryniw | Supervisor: Emmanuel Mapfumo
(Department of Biological and Environmental Sciences, Concordia University of Edmonton)

Carbon sequestration is the process of long-term carbon storage in the soil. The objective of this work was to investigate how carbon is stored in the soil before biosolids are applied. Understanding how carbon is sequestered in soils will be important in predicting how the application of biosolids will affect carbon sequestration. The difference between the quantity of organic matter and 13C stable isotope was investigated for both low and high pH soils in the coarse soil fraction (>75um) which represents sand particles and macroaggregates, and in the fine soil fraction (<75um) which represents silt and clay particles and microaggregates. Soil samples were collected in a quarter section in Hilliard AB in the summer of 2020. Loss on ignition test and 13C stable isotope analysis was completed. The fine fraction was found to contain a significantly ($P<0.05$) higher percentage of organic matter and organic carbon indicating that the fine fraction is the main driver of organic carbon sequestration in soils. The lower pH soil was also found to have a significantly ($P<0.05$) higher organic matter % and total organic carbon than the higher pH soil. The lower levels of organic matter in the high pH soils could be due to the high pH promoting solubility in organic matter, making it easier to decompose and therefore lowering the organic matter content. There were no significant differences in the coarse and fine fractions or the higher vs. lower pH soils for the 13C stable isotope ratio testing.

This suggests that the decomposition rates of organic matter may not be different between fine vs. coarse soil fractions. In conclusion, this study shows the importance of taking into account the soil fraction sizes in organic carbon sequestration.

ENVSCI-02

EVALUATING THE LATE PLEISTOCENE AND EARLY HOLOCENE ARCHAEOLOGICAL POTENTIAL IN WEST-CENTRAL ALBERTA: A GEOMORPHOMETRIC APPROACH

Ben Michalchuk | Supervisor: Robin Woywitka
(Department of Physical Science, MacEwan University)

West-central Alberta is a part of what has been dubbed the Ice-Free Corridor (IFC), a region defined as the earliest sections of ice-free land within continental Canada in the latter end of the late-Pleistocene. There is recent evidence to suggest the IFC may have been biologically viable at least ca. 13,000 years ago but the history of its earliest human occupation is contentious and dedicated explorations to find Late Pleistocene/Early Holocene across the IFC are limited. The available archaeological record is limited, as known sites with well stratified or deeply buried deposits are rare. This is paired with a paucity of organic materials in these deposits, further inhibiting the establishment of the cultural chronologies of the corridor. To address this issue, a process-depositional model is being proposed as a tool for the assessment for archaeological potential and surveys. The process-depositional model developed recognizes the elevated depositional potential of soils atop topographies with concave geometries along the lower margins of raised landforms; a potential amplified for those geometries on the leeward side of such landforms. Assuming this, it is recommended that current survey strategies be adapted to sample a wider variety of landforms and landform elements, where physical location and geometry would positively influence soil deposition. Incorporating high resolution digital elevation models, detailed surficial geology mapping, and archaeological survey information-landscape settings and sedimentary contexts where early archaeological sites are likely to be preserved were mapped. The resulting product will serve future surveys for Late Pleistocene/Early Holocene archaeology in the IFC.

ENVSCI-03

SPATIAL ANALYSIS OF PERMAFROST THAW ALONG THE OLD CROW RIVER: EXPLORING CONTROLS ON RETROGRESSIVE THAW SLUMP ACTIVITY AT A REGIONAL SCALE

Brooklyn Miller | Supervisor: Rui Hu
(Department of Physical Sciences & Mathematics and Statistics, MacEwan University)

The Old Crow River flows across a continuous permafrost zone in the Northern Yukon, where seasonally frozen ground contains ice, organics, and metal pollutants. Retrogressive thaw slumps can form on the river terrace when permafrost thaws and sediment flows downslope into the river, leaving a large unvegetated scar in the terrain. A thaw slump will rapidly grow until stabilization processes impede permafrost thaw, but the controls on these processes vary throughout the Yukon and have not been studied along the Old Crow River.

A dataset of environmental and geomorphic measurements at over 200 thaw slumps along the Old Crow River was created using satellite images (QuickBird-2 & Sentinel-2) and digital elevation data. Preliminary data exploration suggested that river sinuosity, slope direction and steepness, moisture stress, and proximity to certain landforms might influence the growth and stabilization of a thaw slump. These hypotheses are further tested through spatial analysis using statistical language R to determine the relationship between the proposed variables and thaw slump activity.

ENVSCI-04

NUTRIENT-DRIVEN BIOEROSION IN THE DEVONIAN REDWATER LEDUC FORMATION REEF

Phoenix Rowley | Supervisor: Hilary Corlett
(Department of Physical Sciences, MacEwan University)

The Leduc Formation (LF) reefs formed in the Devonian in the Western Canadian Sedimentary Basin (WCSB). The LF reefs were dominated by stromotoporoid, rugose and tabulate corals. The punctata Event was marked by the formation of the world's first forests and development of more complex root systems that resulted in physical erosion of rocks and development of soils. Increased runoff of the soils into the ocean can cause eutrophication which can lead to oceanic anoxia or increased oxygen stratification. There is evidence of increased cementation and microbes in the Leduc Reef which could be an indication of periods of environmental stress. There is also evidence of changes in bioerosion throughout the reef which is known from modern day settings to be a proxy for increased nutrients. Evidence of micritization, and micritic envelopes, were recorded to make a map of bioerosion through the core.

The current research project investigates the relationship between bioerosion and increased nutrients and if there is a potential link to the demise of reefs leading up to the Frasnian/Famennian extinction, one of the big five extinctions in Earth's history. To evaluate changes in bioerosion and Renalcis microbe content throughout the reef thin sections have been analyzed in a petrographic microscope and the degree of bioerosion has been recorded and ranked from 1-5, reflecting the intensity of bioerosion. Renalcis content was recorded to map where these microbes were present or absent. Preliminary results have shown that the middle portion of the reef shows higher degrees of bioerosion, which corresponds to the carbon isotope markers that signal the onset of the punctata Event.

This study will help encourage further research on this topic and hopefully create a timeline to better explain when the punctata Event occurred and what effects it had on decreased growth of the LF reefs during the Devonian, leading up to the Frasnian/Famennian Extinction Event.

ENVSCI-05

MAPPING EARLY DIAGENETIC ALTERATION IN CARBONATE GRAINS FROM ABU DHABI USING RAMAN SPECTROSCOPY

Radhika Saini | Supervisor: Hilary Corlett
(Department of Physical Sciences, MacEwan University)

Raman spectroscopy is an effective and non-destructive method for distinguishing between carbonate minerals. Though similar, the spectra of aragonite, calcite, and dolomite each display subtle differences in peak positions, which is ideal for differentiating these minerals within a single grain that may have experienced early diagenetic alteration. Depositional features and early diagenetic alteration are often overprinted and difficult to recognize once sediments are lithified and buried, where pressure, temperature, and subsurface fluids impart further diagenesis. Since we are not always able to recognize early diagenetic alteration, various specimens have been lost from this process, which skews our current record of fossil populations. For example, most molluscs precipitate aragonitic shells, which are particularly prone to diagenetic alteration in the form of dissolution or alteration to the more stable calcite polymorph. This study aims to identify signs of early diagenesis in carbonate ramp sediments from Abu Dhabi by detecting aragonite and calcite transformation using Raman spectroscopy. Thin sections prepared from the Abu Dhabi sediment cores are used to create 2D maps of grains subjected to bioerosion and early diagenesis. The maps depict an explicit transformation between aragonite and calcite as the Raman spectra contains both calcite and aragonite peaks in the transition zones of various maps, including alteration along the edges of grains that have experienced mechanical boring. Micrite along the edges of bored grains is indistinguishable from the surrounding carbonate mud. Mapping the early alteration of carbonate sediments will aid in our interpretation of the fossil record as we can better understand what grains may have dissolved or been incorporated into the sediment through micritization versus grains that have been preserved through alteration of unstable aragonite to more stable calcite.

ENVSCI-06
CHARACTERIZATION OF LONG-TOED SALAMANDER MICROHABITAT STRUCTURE IN SOUTHWESTERN ALBERTA PRIOR TO A MAJOR WILDFIRE

Tristan Skretting | Supervisor: Julie Lee-Yaw
(Department of Biology, University of Lethbridge)

Amphibians are in decline globally and are primarily threatened by habitat loss and degradation. Understanding the effects of disturbance on amphibian populations requires a baseline knowledge of their habitat needs. In this study, I characterize and describe microhabitat structure at different distances away from Long-toed Salamander (Ambystoma macrodactylum Baird, 1850) breeding ponds in Waterton Lakes National Park, Alberta prior to a severe wildfire. In addition to distance from the pond edge, I specifically examined microhabitat variation in relation to the boundaries of the 2017 Kenow wildfire, allowing for assessment of potential unique habitat loss as a result of this disturbance. Cover or substrate type immediately adjacent to pond edges was characterized by large amounts of herbaceous material, litter, woody-stemmed vegetation, and bare ground. As distance from pond edge increases, woody vegetation increases and bare ground decreases. There were no differences in microhabitat structure between sites that were subsequently burnt and those that were not. Overall, these results provide a baseline understanding of microhabitat for this and other co-distributed species prior to a severe wildfire and suggest that pond habitats impacted by Kenow were not particularly unique in the park.

SESSION C3 | 1:30 PM - 4:30 PM

HS-16
ASSESSING MEDICAL ABORTION ACCESS IN CANADA

Katrina Taylor | Supervisor: Jean Harrowing
(Department of Biological Sciences, University of Lethbridge)

Almost 1 in 3 Canadians who can become pregnant will have at least 1 abortion in their lifetime. However, abortion services are very limited in Canada, and almost exclusively located in urban areas. The low accessibility of these clinics disproportionality affects rural, vulnerable and/or low-socioeconomic patients, for whom the cost, traveling distance and increased time requirement negatively burden. This study surveyed physicians practicing in Alberta, Saskatchewan, Nova Scotia, PEI and Nunavut through their respective provincial medical association newsletters. It investigated facilitators and barriers influencing a physician's willingness and perceived ability to engage with a patient seeking a medical abortion. We found physicians generally rated their knowledge of current prescribing and dispensing information and confidence prescribing as low. This study highlights the lack of medical abortion access in Canada and factors physicians perceive as influencing their ability to engage with a patient wishing to terminate their pregnancy through a medical abortion.

OTHER-04
SALIVARY METABOLOMIC BIOMARKERS INDICATIVE OF STRESS VULNERABILITY AND RESILIENCE IN SYRIAN REFUGEES

Steel McDonald, Laisa Kelly, Tanzi Hoover, Tony Montina | Supervisor: Gerlinde Metz
(Department of Neuroscience, University of Lethbridge)

Refugees arriving from conflict zones often continue to experience trauma and are at risk for post-traumatic stress disorder. Those seeking asylum form a group at risk of suffering mental health disorders, for whom psychosocial and therapeutic care is required. This study investigates whether proton nuclear magnetic resonance (1H NMR)

can identify metabolomic biomarkers that indicate stress vulnerability and resilience in Syrian refugees. Earlier research has shown that metabolomic profiles are able to identify a "metabolic fingerprint" that aids in biomarker indications in a cost-effective assessment and non-invasive sample collection technique. Participants were recruited from Lethbridge Family Services and divided into groups of high and low stress based on fifteen questionnaires that were used to measure stress, history of adverse experiences, depression, discrimination, and resilience. These questionnaires include tests for anxiety (GAD-7), depression (PHQ-9-15), and resiliency (Connor-Davidson) to name a few. In this study, we investigated the metabolomic salivary profiles taken from 27 female and 32 male participants, looking directly at the metabolomic comparisons of composite stress, depression, and anxiety. Metabolomes across participants were determined to show differences in the salivary profiles of high and low stress, predominantly in females. 24 metabolites were considered significantly altered according to multivariate statistical analysis and 1H NMR spectroscopy. 18 biological pathways were impacted with the most noticeable being glycolysis/gluconeogenesis, sphingolipid metabolism and glycerophospholipid metabolism. These results suggest that metabolomic techniques using 1H NMR may be an effective method to understanding stress vulnerability and resiliency in Syrian refugees. Thus, this research will provide decision making tools to identify vulnerable individuals who are at the greatest risk and in need of special social or medical support.

OTHER-05
HOW DOES BEING SICK IMPACT LEARNING IN A SOCIAL SETTING?

Parker McNabb, Chelsea Matisz | Supervisor: Aaron Gruber
(Department of Neuroscience, University of Lethbridge)

Background: Observational learning consists of a behaviour being learned and implemented after watching a conspecific perform the behaviour. This type of learning is evolutionary advantageous; observational learning enables animals to identify rewards and threats rather than having to learn through trial and error, which can be costly. But how does the health of the animal being observed play a role in this type of learning? Inflammation drives well-established sickness behaviours in mice, including changes to reward sensitivity and threat assessment. The purpose of this experiment is to test how chronic and acute peripheral inflammation in mice influences learning in a social setting.

Methods: To test this hypothesis we use an observational learning predator/prey task as a model for social learning. Demonstrator mice are trained to interact with a wax puck associated with a reward, or a wax puck associated with a threat (chase). Controls and mice with either acute or chronic gut inflammation observe trained demonstrator mice as they interact with the wax puck in the reward or threat context. Mice were administered dextran sodium sulfate (DSS) in their drinking water to induce gut inflammation through a mouse model of colitis.

Results/Conclusion: Controls exposed to the positive context interacted with the wax puck in an appetitive way. Controls exposed to the negative context responded to the puck as an aversive stimulus. We expect that mice treated with acute or chronic gastrointestinal inflammation to have a learning bias in response to either the positive or negative context. We predict the learning bias to manifest as greater learning sensitivity in the negative context when compared to the positive context. We hypothesise that the biased response of the treated mice to be the result of changes in their affective state; these changes may bias the learning system to be more sensitive in a negative social learning setting.

OTHER-07
REACH & GRASP: TWO SEPARATE MOVEMENTS OR JUST ONE?

Maleeha Panjwani | Supervisor: IanWhishaw
(Department of Neuroscience, University of Lethbridge)

Human right-handed subjects between the ages of 21 to 35 years participated in three different tasks, all involving various aspects of reaching and grasping. Females did better than their male counterparts at two out of the three tasks. Two out of the three tasks were performed superiorly by the subjects' right hands than their left hands which promotes support for the finding that hand dominance plays a role in the accuracy of reach and grasp movements.

OTHER-08

INVESTIGATING THE DYNAMIC ACTIVITY OF NEUROMODULATORS (NA, ACH, DA, 5-HT) DURING CUE-BASED LINER TRACK EXPLORATION

Bailey Porter, Setare Tohid, Mojtaba Nazari, Majid Mohajerani | Supervisor: Bruce McNaughton
(Department of Neuroscience, University of Lethbridge)

Cognitive functions are processes that enable us to think, learn, and remember and are critical for healthy ageing. Mammalian behaviours and cognitive functions are regulated by neuromodulators such as Acetylcholine (ACh), Dopamine (DA), Noradrenaline (NA), and Serotonin(5-HT). Neuromodulators (NM) are slowly released from neuromodulatory systems situated in the subcortical regions such as brainstem, basal forebrain, and pontine nuclei and evoke long-lasting effects on downstream targets. NMs play a role in diseases such as Alzheimer's disease, contributing to the decline in cognition and memory and behavioural issues such as anxiety and depression. Although there is a general understanding of the functions of various NM, there are limited studies that have looked at NM activity in-vivo across the cortex. The four neuromodulators explored in this study are ACh, DA, NA, and 5-HT, whose known functions are modulating memory and attention; reward prediction and characterizing novel inputs in the environment; reorganization of the brain due to surprise and brain state regulation; and predicting punishment and harm aversions, respectively. By using widefield transcranial calcium fluorescent imaging, we recorded axonal and terminal activity within the neocortex of the following healthy transgenic mice groups: Ai162 x Chat-cre, Ai162 x Dbh-cre, Ai162 x Th-cre, Ai162 x Slc6a4-cre, following chronic window implantation along with hippocampal and electromyography electrodes. Mice were habituated to be head-fixed while running on a cue-based liner belt with an air-puff aversive stimulus and milkshake reward. We then introduced novel visual and tactile cues during which electrode signals, neural activity, pupillary responses, and behavioural data were collected and analyzed. This study aims to bridge the knowledge gap surrounding the activity of NM in-vivo, with the future direction of replicating the study in Alzheimer's Disease models.

OTHER-12

THE METABOLOMIC PROFILE OF ALZHEIMER'S DISEASE IN HIPPOCAMPAL BRAIN TISSUE

Giselle Tiede | Supervisor: Gerlinde Metz
(Department of Neuroscience, University of Lethbridge)

To date, Alzheimer's Disease (AD) can only be accurately diagnosed post-mortem by observing characteristic morphological traits in the brain, including amyloid plaques and neurofibrillary tangles. In addition, most patients do not present clinical symptoms typical of the deterioration of mental state associated with AD until further in the disease's progression, thus making early detection nearly impossible. Accurate early diagnosis methods would allow for more specialized care geared towards AD and more effective personalized and preventative treatments.
 The aim of this metabolomics-based study of AD was to identify cellular changes that can potentially be used in early diagnosis of AD. Metabolomics is the quantification and identification of the metabolome present in cells, tissue, and biofluids. The metabolome is a representation of all down-stream small molecules produced by various cellular activity. A better understanding of changes in the brain's metabolome will result in a more precise idea of what biomarkers of AD may be detected elsewhere in the body.

Nuclear magnetic resonance (NMR) spectroscopy is an ideal tool for quantifying and comparing the metabolomic profiles of tissues associated with AD. In this study, we investigated the metabolomic profile of the hippocampus, a brain region that is essential for memory. Brain tissues were obtained from the Calgary Brain Bank and categorized as either AD (n=11) or control (n=11). Using univariate, multivariate, and machine learning analysis, we identified 47 specific metabolites that could accurately classify AD versus non-diseased tissue. Biochemical pathways that are potentially affected are: aminoacyl-tRNA biosynthesis, valine, leucine, and isoleucine biosynthesis, and alanine, aspartate and glutamate metabolism. These results provide new insights into the mechanistic changes that may underly AD pathology and provides targets for future studies of downstream and accessible biomarkers, such as biofluids.

Oral Presentation Schedule

A special thanks to our sponsors and a big thank you to all who supported and encouraged us in the planning and delivery of this conference.

Keynote Speaker

Dr. Alejandro Adem, NSERC President

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Adrienne Benediktsson	Janice Kenney	Ramses Ilarraza
Alesha Reed	Jean-Denys Hamel	Raphael Slawinski
Angela Cullum	Jeella Acedo	Rashmi Panigrahi
Briana Boychuk	Jenni Scott	Robin Woywitka
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Crystal Snyder	John Chik	Sarah Hirtle
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