2012

POSTER PRESENTATION ABSTRACTS

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Comparing Seepage Meter and Piezometric Methods of Measuring Groundwater Discharge

Student: Craig Baptie
Supervisor: Dr. Craig Nichol

Groundwater discharge is an important component of groundwater-surface water interaction and its quantification is necessary for accurate groundwater modeling. This study compares seepage meters and piezometric methods as means of measuring groundwater discharge into Okanagan Lake. Seepage meters are commonly used to directly measure the volumetric discharge across the sediment-water interface. The piezometric method involves calculating volumetric flux using Darcy's law with measurements of hydraulic gradient and hydraulic conductivity. The advantage of this method is it can be performed more easily in deep water than the installation of seepage meters. This study compares results at 16 sites identified as areas of high or medium flow. At each site, a seepage meter measured flux over 24 hr periods. Following removal of the seepage meter, piezometers were installed at depths of 0.3 m and 1.00 m below the sediment-lake interface to measure vertical hydraulic gradient. Hydraulic conductivity was measured by in-situ falling head tests and laboratory permeameter tests. The results from this study may allow for the two methods to be used interchangeably as part of a project to quantify groundwater discharge into Okanagan Lake from the Kelowna aquifer.

Synthesis and Characterization of Bis(oxazolinylpyrrolyl)cobalt(II) Complexes for Controlled Radical Polymerization

Student: Justin Black
Supervisor: Stephen McNeil

Polymerization reactions are important to today's society and modern chemistry because such processes permit the creation of many modern materials, most recognizably plastics. Currently, many industrial polymerization reactions are controlled using 2nd and 3rd row transition metal catalysts. These catalysts are often harmful to the environment, toxic, and expensive, and they are largely incompatible with the precursors to many large-scale polymers, such as those with polar sidechains. Such molecules, including vinyl acetate, are still best best-polymerized via a radical process, but radical reactions are generally uncontrolled, leading in turn to poor control over the resulting polymer properties. By using cobalt mediated radical polymerization (CMRP) these problems are largely avoided and thus CMRP is a desirable method by which to conduct polymerizations of molecules like vinyl acetate. A series of tetrahedral bis(oxazolinylpyrrolyl)cobalt(II) complexes have been synthesized and characterized by X-ray crystallography, paramagnetic ^{1}H-NMR, and UV/visible spectroscopy. The ability of these complexes to mediate the radical polymerization of vinyl acetate under different mechanistic conditions has been examined, and compared to that of structurally-similar bis(aryliminopyrrolyl) complexes. Polymerization rates and degree of control can be related to variation of electronic and steric properties of the designed ligands and the exact mechanistic role of varying ratios of cobalt mediator to radical initiator have been explored.

Modelling *Botrytis cinerea* growth as a function of enzymatic and metabolic parameters

Student: Haley Dirksen
Supervisors: Dr. Cédric Saucier, Dr. Louise Nelson, Dr. Rebecca Tyson

Botrytis cinerea, a necrotrophic fungus, is the causative agent of two types of rot in grapes used to make wine: bunch rot (detrimental) and noble rot (advantageous). Several chemical and enzymatic compounds are produced by *B. cinerea* throughout the course of infection and, as such, are implicated in the development of both forms of rot. The aims of our research were three-fold: (1) To assess the effect of glucose, gallic acid, and gluconic acid on fungal growth and the production of the enzyme laccase by *B. cinerea*; (2) To develop and refine a mathematical model capable of predicting the change in glucose, gallic acid, gluconic acid, and laccase with respect to the growth rate of the fungus; (3) To use the mathematical model to elucidate the mechanisms behind laccase activity. A novel procedure was developed to extract laccase from the growth medium in a reproducible manner with a high percent recovery. The activity of the enzyme was then quantified using a UV-Vis spectrophotometer. This method was used to determine the laccase activity with respect to the amount of gallic acid present in the growth medium. Ultra High Pressure Liquid Chromatography (UHPLC) analysis was then performed in order to quantify the amounts of glucose, gluconic acid, and gallic acid present with respect to the duration of growth. These results were then compared with the mathematical model simulations to ascertain the efficacy of the model.

Paper Spray Ionisation for the Analysis of Naphthenic Acids

Student: Felicia Douglas
Supervisor: Dr. Rob O'Brien

Naphthenic acids are polar organic compounds that are found within crude oil and subsequently oil sands process water (OSPW). The structure can be described by the formula $C_nH_{2n+z}O_2$, where *n* is the number of carbon atoms and *z* denotes the hydrogen deficiency in the case of cyclic naphthenic acids. Corrosion of oil refinery equipment is a primary concern as well as further contamination of surface waters and groundwater, resulting in toxicity to a wide range of aquatic biota. The current methods used to both quantify and characterise these very complex compounds are not extensively developed. We are proposing to use a relatively new technique called paper spray ionisation as a potential analytical method for the analysis of naphthenic acids. Paper spray is an ambient ionisation technique that is advantageous for this particular analyte. As a soft ionisation technique minimal fragmentation occurs, which allows for such ions as $[M - H]^-$ and $[M + H]^+$ to be observed in the negative and positive-ion mode respectively. Coupled with mass spectrometry, paper spray has been demonstrated as both a rapid and convenient method for direct analysis of complex matrices. Unlike electrospray ionisation, which is quickly becoming the industry standard for analysis, paper spray offers some obvious advantages to the study of naphthenic acids. This technique can use both polar and non-polar solvents, eliminate sample cross-contamination, and does not require any sample pre-treatment. Water samples

were obtained from the Athabasca oil sands region and included OSPW and groundwater samples. This project looked to evaluate the analytical performance of the instrument through quantification of naphthenic acids and gain insight into the mechanisms of paper spray ionisation by analysing this class of compounds.

Finding the Molybdenum Transporter in Rainbow Trout: Direct quantification using ICP-MS analysis

Student: Courtney Ek
Supervisor: Dr. Scott Reid

Molybdenum (Mo) has been shown to be toxic in many terrestrial animals including cattle and rats (Telfer et al., 2004; Vyskocil and Viau, 1999), but how does this heavy metal affect aquatic organisms? Since molybdenum is used commonly in industrial processes to produce fertilizers, rubber, paints, lubricants and metal alloys, it is not surprising that it has become a contaminant of real concern. This is especially important in aquatic environments where organisms tend to be more sensitive to changes in their environment. In an effort to learn more about the way Mo interacts with freshwater fish, this study sets out to directly determine the specific site of molybdenum transport in fish gills. First, a digestion protocol was developed using whole tissue samples from rainbow trout (*Oncorynchus mykiss*; plasma, gill, white muscle, and liver). Then the gills of six additional fish were collected (three control and three exposed; 20 mg/L Mo) and separated into pavement cells (PVC), and two types of mitochondria-rich cells (MRC; PNA+ and PNA-) using a method modified from Galvez et al. (2002). The concentrations of molybdenum within these samples were measured using an inductively-coupled plasma-mass spectrometer (ICP-MS). Pavement cells are believed to be responsible for gas exchange while MRCs are important in ion transport, much like the mammalian kidney. With this in mind, I predicted the MRCs would contain more molybdenum than the PVCs. A previous honours student, using indirect methods of molybdenum quantification in rainbow trout, concluded that the PNA+ cells were the main site of Mo transport in the gills. My results, using direct methods of molybdenum quantification, support the findings of the previous study and my hypothesis.

Pseudomonas fluorescens isolates 1-112 and 4-6 as viable biocontrol agents for postharvest decay of d'Anjou pears

Student: Karen Fong
Supervisor: Dr. Louise Nelson

Postharvest disease is a serious issue around the world causing detrimental effects on crop quantity and quality. Postharvest pathogens are usually present in the field and infection starts as a result of wounding or rough handling during harvest and processing. In the Okanagan, pears (*Pyrus communis*) are commonly infected with three fungal pathogens: *Penicillium expansum*, *Botrytis cinerea*, and *Mucor pyriformis*. Although chemical treatments are often used to kill these pathogens, there is concern about their use due to possible adverse health effects. Biological alternatives have been studied as a possible

strategy for reducing postharvest decay. Microorganisms are applied to the surface of the fruit and can effectively limit or inhibit fungal growth.

Pseudomonas fluorescens has not been extensively studied as a biocontrol agent for postharvest pathogens. This study examined the ability of *P. fluorescens* isolates 4-6 and 1-112 to control postharvest decay of d'Anjou pears in two different storage conditions, cold storage and controlled atmosphere (CA) storage. Fungal pathogens *P. expansum*, *B. cinerea* and *M. pyriformis* were grown on potato dextrose agar and spore suspensions of 10^4 spores/mL were prepared and co-inoculated into wounded pears with 10^8 CFU/mL of isolates 1-112 and 4-6 grown in tryptic soy broth. Pears were stored for three months at 4°C and infection was measured at monthly intervals. Both isolates of *P. fluorescens* effectively limited fungal growth in cold storage, as measured by infection severity. Preliminary measurements after three months indicated that isolates 1-112 and 4-6 were also effective in controlling decay of pears in CA storage. This may be due to the production of siderophores, anti-fungal metabolites or through direct competition for nutrients in the pear fruit. These data suggest that *P. fluorescens* may have potential for control of postharvest fungal pathogens of pear fruit during cold and controlled atmosphere storage.

Expression and isolation of soluble 3-phosphoshikimate 1-carboxyvinyltransferase (EPSPS)/acyl CoA ligase from *Streptomyces nodosus* ssp*. Asukaensis*

Student: Nichole Gill
Supervisor: Dr. Mary Forrest

Asukamycin is a novel manumycin-group metabolite produced by *Streptomyces nodosus* ssp. *asukaensis* which has been found to have antimicrobial, antifungal, anticoccidial, and potential antitumor activities. By blocking the synthesis of a crucial asukamycin intermediate such as the unique cyclohexane carboxylic acid (CHCA) moiety via mutation and providing the culture with various analogues, it may be possible to generate novel bioactive compounds. Sequence data indicate that the ORF 23/24 gene from *Streptomyces nodosus* ssp. *asukaensis* encodes a unique, bifunctional 3-phosphoshikimate 1-carboxyvinyltransferase (EPSPS)/acyl CoA ligase which is believed to catalyze the first two steps of CHCA production. This project studied expression of the ORF 23/24 gene; which had been previously cloned into an expression vector, while optimizing extraction of the EPSPS/acyl CoA ligase product from expression host cells. The effects of altering *E. coli* growth conditions and IPTG induction times were studied and various protein solubilization techniques were investigated. Purifying the EPSPS/acyl CoA ligase in a soluble and enzymatically active form will allow for analysis and testing of enzyme activity using various assays. Study and characterization of the EPSPS/acyl CoA ligase will allow for an increased understanding of the mechanism and function of this unique enzyme and the possibility to explore production of asukamycin analogues and novel compounds with potentially increased bioactivity and medical relevance.

Implicit Theory Structures of Psychopathy

Student: Cailey Alexis Gilmurrary
Supervisor: Brian P. O'Connor

A basic assumption that has guided the many investigations of the dimensional structure of psychopathy has been that the results of such studies are reflections of the structure of the psychopathic traits and behaviors of the persons being rated. For the Psychopathy Checklist-Revised (PCL-R; Hare, 2003), trained experts provide ratings for a number of offenders, the ratings are factor analyzed, and the results are presumed to be reflections of the organization of the traits and behaviors of the targets. However, it is common in such studies for there to be only a small number of experts who provide the ratings for all of the offender targets, and the factor analyses are usually conducted on the ratings provided by just one or a small number of experts. It is therefore possible that the structures that are revealed by such investigations are reflections of the implicit beliefs of the raters. In the present study, we examined, using a sample of 159 respondents, whether previously published dimensional structures for the PCL-R that have emerged when offenders have been rated can be replicated from a data set wherein participants merely rated the degrees of semantic similarities between all possible pairs of PCL-R items. The findings from factor analyses and from multidimensional scaling analyses revealed substantial (.80 range), although not perfect similarities between the real person data and the semantic similarity data. It is concluded that PCL-R factor structures from offender-based data sets are at least partly reflections of the implicit beliefs of the persons who provide the ratings.

Expression of the Bifunctional EPSPS/Acyl-CoA Ligase Enzyme from ORF23/24 of *Streptomyces nodosus* ssp*. asukaensis*

Student: Jill Gilroy
Supervisor: Dr. Mary Forrest

Production of secondary metabolites from microorganisms accounts for up to two thirds of known antibiotics, of which nearly 80% are made by members of the genus *Streptomyces* (Kieser et al., 2000). *Streptomyces nodosus* ssp*. asukaensis* produces a unique manumycin compound, asukamycin, which makes is distinct from other manumycins by the presence of a cyclohexane carboxylic acid side group. Expression of the ORF 23/24, which codes for an enzyme of dual functionality involved in the catalytic synthesis of the unique side group, is examined in this study. The ORF23/24 has been cloned into the expression vector pGS-21a and replicated in the *Escherichia coli* BL21-DE3 expression host. Methods of expressing and extracting the product were implemented and supernatant and pellet components of lysed cells were analyzed for presence of the ORF 23/24 product. Currently, extracting the protein in a soluble form has been unsuccessful and the gel analysis of the cell fractions has not revealed sufficient manifestation of the expression product. Once expression has been improved, isolation of the protein will be implemented by utilizing the GST and 6xHis-tags incorporated into the expression vector. After

attaining the product in its purified form, the intent is to examine the functionality of the enzyme through its incorporation into enzyme assays.

Tissue expression patterns of the passive copper transporters *ctr1b & ctr1u* in larval *Aedes aegypti* following 24 hour exposure to water borne copper

Student: Matt Glover
Supervisor: Mark Rheault

The transition metal copper is an essential trace element that is critical to the metabolic function of all eukaryotic organisms. Copper is utilized as a cofactor for a number of metabolic enzymes, such as cytochrome C oxidase, which is essential for ATP synthesis. A number of copper transporting proteins that are responsible for copper regulation have been identified in various vertebrate and invertebrate species. The SLC31A superfamily (CTR family) includes high affinity copper uptake transporters. In the yellow fever mosquito, *Aedes aegypti*, two putative *ctr*-like genes (Ctr1b & Ctr1u), orthologous to human and *Drosophila melanogaster* transporters have been identified and called in this study *ctr1b* and *ctr1u*. The mRNA expression profiles of *ctr1b* and *ctr1u* were examined using quantitative real-time polymerase chain reaction (qPCR) in 4th instar larva of *A. aegypti*. Larva were exposed to 0.5 and 2.0 mmol l^{-1} Cu^{2+} and the expression of both *ctr1b* and *ctr1u* were measured relative to unexposed controls. Whole body, midgut, Malpighian tubules, hindgut and anal papillae tissues were tested. These tissues represent structures previously demonstrated to be responsible for ion regulation in insects. We found that *ctr1b* was constitutively expressed in all tissues tested, and expression was unaffected by copper exposure. Whereas *ctr1u* expression was highly dependent on external levels of copper with expression increasing over 4000-fold in Malpighian tubules relative to whole body following 24h exposure to 2.0 mmol l^{-1} Cu^{2+}. The results of this research expand current knowledge on how transition metals such as copper are regulated in insects. This study supports the development of *A. aegypti* as an invertebrate bio-indicator species for aquatic environmental metals toxicity.

Physical Factors Affecting Infrared Thermography as an Early Disease Detection Method in Cattle

Student: Paige Hegadoren
Supervisors: Dr. Mark Paetkau and Dr. John Church
(Thompson Rivers University – Department of Physics)

Bovine respiratory disease is a common and costly disease in the cattle industry with respect to both treatment costs and negative impacts on animal welfare. Elevated body temperature in cattle is an early indicator of infectious disease; other clinical symptoms occur later in the course of the disease, at which time the disease may have spread. Quick, convenient and accurate body temperature measurements are desirable for early disease detection. Infrared thermography (IRT) involves the use of infrared cameras to infer surface temperatures based on infrared (IR) radiation. Unlike traditional temperature measurement methods, IRT is a non-invasive procedure. It has been suggested that an IR image of the

eye could indicate body temperature. In this study we investigated the physical and environmental factors affecting IRT in order to construct a physical model for IRT measurements to increase accuracy. We studied the effect of camera-object distance, camera-object angle, and ambient wind speed on surface temperature read by the IR camera. We found a linear relationship between camera-object distance and surface temperature, as well as a linear relationship between wind speed and surface temperature. The linear relationship is a classic, simple relationship which we can easily model for. We found the effect of camera-object angle to be negligible. In order to be a reliable diagnostic tool, IRT needs to be an accurate proxy for cattle body temperature. By understanding these physical factors, we may be able to account for them in IRT measurements involving early diagnosis of febrile cattle, ultimately trying to improve diagnostic success.

Landslide Susceptibility in the Quesnel Area, British Columbia: A Weight-Indexing, Qualitative Mapping Technique (GIS Based Assessment)

Student: Chris Jahnig
Supervisor: Dr. David Scott

Mass movement, or landslides, have been the source of much economic and social cost and is a significant factor to consider in development of infrastructure. These hazards have been studied and assessed world-wide but is still a relatively young and unexplored topic of study in Canada. This project combines information regarding landslides (triggers, conditioning factors, prone locations, etc.) to map out areas that may be prone to landsliding. The study uses a qualitative, susceptibility mapping method to assess landslide risk for the map unit encompassing the town of Quesnel, British Columbia and surrounding area. The technique, weight indexing, attempts to zone areas that may be liable to to mass movement events based on few parameters. Parameters were selected and chosen based on usage from past studies by experts in the study of landslides and the data that was available on the respective factors.   The parameters that were decided upon slope angle, drainage of soil, aspect of slope, land use types, and mode of deposition. Data that was used came from CanSIS (Canadian Soil Information Systems), for soil data, and slope, aspect and elevation data was taken from HectaresBC. Factors were given a weight (out of 1), determined from past studies, depending on their relative influence on landsliding. The parameters were added as data layers in GIS and converted into raster format and a susceptibility index was developed and calculated using a raster calculator on the QuantumGIS software program. The susceptibility maps created are essential for landzoning and development in avoiding unsafe environment conditions. The areas within the Quesnel region that were most susceptible to landslides were close in proximity to slopes carved by meandering rivers and of poor water drainage.

Alternative Conceptions of Bonding Models among Second Year Chemistry Students: When Bonding Models Collide

Student: Johnathan D. Kohout
Supervisor W. Stephen McNeil

Chemistry students often develop mistaken impressions as the use of various molecular bonding theories, which can limit their understanding of later courses. A quasi-experimental study was undertaken, using pre- and post- exercise assessments between control and experimental student groups in a second year organic chemistry class, in order to identify students' alternative conceptions of bonding, and to establish the effectiveness of an in-class exercise called "Duelling Bonding Theories" (DBT) at correcting them. Guided-inquiry interviews were also performed to further examine student alternative conceptions. It was found that when DBT was used in conjunction with a course that consistently emphasized the strengths and differences between molecular bonding theories there was a statistically significant increase in student understanding and a decrease in alternative conceptions. It was also found that many alternative conceptions involved misunderstandings about the limitations of a given model, leading to attempts to use simple models to explain properties for which they were not designed. We also found that many students attempt to interpret molecular behaviour in terms of the properties of isolated atoms, rather than in terms of electrons shared among interatomic bonds or molecular orbitals.

A Petrological Analysis of Pegmatitic Rocks from Wadi Qutabah, Yemen.

Student: Mark Lam
Supervisor: Dr. John D. Greenough

The study describes the mineralogy and garnet chemistry of a pegmatite body found in the Wadi Qutabah area of Yemen in an effort to unravel the petrogenesis of the rocks. The pegmatite body was sampled at depth using diamond drilling. Petrographic and macroscopic examination shows that the pegmatites are extremely coarse-grained rocks (>30cm grain size in some samples) with distinct graphic intergrowths of quartz and microcline. The simple mineralogy also includes albite, garnet, minor muscovite, and biotite. The extremely large crystal sizes make whole rock geochemical characterization of the pegmatite unreliable: the data could be highly influenced by sampling and not necessarily representative of the pegmatite body. Instead, laser ablation inductively coupled plasma mass spectrometry (LA-ICPMS) is used to describe the trace element (Cs, Rb, Ba, Th, U, Nb, Ta, La, Ce, Pb, Pr, Sr, P, Nd, Sm, Zr, Hf, Eu, Gd, Tb, Dy, Y, Ho, Er, Tm, Yb, and Lu) signature of individual garnet crystals as a proxy for original magma compositions. The aluminous nature of the magma that drove garnet formation suggests the pegmatite formed from an S-type (sediment-derived) granitic magma. Small, negative Ce anomalies, and large negative Eu anomalies on chondrite-normalized rare-earth element diagrams are respectively consistent with melting marine shales with plagioclase as a residual phase after melt extraction. Nb/Ta relationships on primitive-mantle normalized trace element diagrams

resemble those in whole-rock S-type granites where crustal fluids, presumably also responsible for pegmatite formation, fractionate Nb from Ta.

Bioc 448 – UBCO Undergraduate Research Conference Abstract
Student: Allison Low
Supervisor: Paul Shipley

The genus *Crataegus*, or hawthorn, has been long-established as having bioactive metabolites that have been used in natural health products (NHPs) to combat heart failure and improve blood flow. Hawthorn-based NHPs do not distinguish their flower, leaf and berry compositions even though the plant parts are all known to vary in the quantity and composition of compounds. This project aims to compare compound differences of hawthorn flowers between different trees of *C. monogyna, C. heldreichii, C. pinnatifida,* and *C. hupehensis* after a methanol extraction of freeze-dried samples and metabolite fingerprinting by J-resolved nuclear magnetic resonance spectrometry. Additionally, compounds are also compared between the flowers and leaves of the same hawthorn trees. Statistical analyses were carried out using multivariate techniques such as principal component analysis and partial least squares-discriminant analysis. With a better understanding of compounds found in different hawthorn species and plant parts, NHP preparation can be improved upon.

Contribution of electrostatics to radical initiation in a B$_{12}$-dependent enzyme

Student: Chloe Mariani
Supervisor: Kirsten Wolthers

Ornithine 4,5-aminomutase (OAM) from *Clostridia sticklandii* is an adenosylcobalamin (AdoCbl, coenzyme B12)- and pyridoxal L-phosphate (PLP)-dependent enzyme that catalyzes the radical-mediated 1,2-rearrangement of D-ornithine to produce (2R,4S)-2,4-diaminopentanoic acid. Radical chemistry is initiated by homolytic rupture of the Co-C bond in AdoCbl, a chemical step that is enhanced trillion-fold in the enzyme active site. We hypothesize that electrostatic interactions between the protein and cofactor may lead to transition-state stabilization that in turn lowers the energy barrier of Co-C bond homolysis. This hypothesis is based on the crystal structure of OAM which reveals glutamate 338 in position for electrostatic interactions with the 2' OH and 3' OH of the AdoCbl ribose moiety. To evaluate the role of Glu338 in catalysis, it was mutated into an alanine, glutamine, and aspartic acid. Another residue shown to be within hydrogen bonding distance with the adenosyl group is glutamate 81. In a separate study, this residue was substituted for a glycine. Steady-state kinetic assays were used to determine the turnover rate (k_{cat}) of these OAM mutants. The E338A OAM mutant showed a 2400-fold decrease in k_{cat} compared to wild-type OAM. The E338Q and E338D OAM mutants had a 7000- and 6900-fold decrease in k_{cat}, respectively. The E81G mutation had a 15000-fold decrease in activity compared to wild-type OAM. Surprisingly, the smallest decrease in turnover rate occurred for the least

conserved mutation, E338A. These unexpected data may be explained by the placement of one or two water molecules in the void left by absent carboxylate that can coordinate to the ribose and trigger - albeit weakly - Co-C bond homolysis. These data suggest that E338 and E81 enhance catalytic turnover by contributing to electrostatic stabilization of the transition state formed upon Co-C bond homolysis.

Detection and rhizosphere colonization of two phosphorus solubilising bacteria, *Pseudomonas putida* and *Pseudomonas fluorescens* grown in association with apple seedlings

Student: Kersti Ojamaa
Supervisors: Louise Nelson and Mary Forrest

Replant disorder is a complex and universal problem that affects agricultural land worldwide. One of the most important abiotic factors that limits plant growth, and thereby agricultural production, is phosphorus. The importance of phosphorus is due, in part, to its low bioavailability in soils. In this study we looked at means of increasing soluble phosphorus in the rhizosphere by using two strains of phosphorus-solubilising bacteria, *Pseudomonas putida* 2-106 and *Pseudomonas fluorescens* 4-15. The first objective of the study was to insert the vector pAG408, containing genes for kanamycin resistance, gentamycin resistance and a green fluorescent protein, to allow us to differentiate the two *Pseudomonas* bacteria from other naturally occurring bacteria in the rhizosphere. Two approaches were tried, one using *Escherichia coli* (S17-λ pir) and the second using previously transformed bacteria, *Pseudomonas syringae* 2-28 and *Pseudomonas fluorescens* 4-6. Neither approach was successful as the *E.coli* culture was not viable and the extraction methods used for the latter two species did not yield any usable DNA. An alternate approach for bacterial differentiation was taken by selecting for spontaneous rifampicin resistant mutants of both *P. putida* 2-106 and *P. fluorescens* 4-15. To test whether this mutation affected the bacteria's ability to solubilise phosphorus, trials were completed to compare the wild type and mutant strains of both bacteria. This comparison was completed on both liquid and solid media which contained insoluble calcium phosphate as the sole phosphorus source. To assess the survival and colonization of the mutant bacterial strains in the rhizosphere, apple seedling roots were inoculated and grown over a three week period and bacterial counts determined following dilution plating on rifampicin-containing medium. Applications of these phosphorus solubilising bacteria could potentially aid in replant disorders and improve agricultural production globally.

The influence of wind speed on the dispersal of dormant stages of *Artemia franciscana*

Student: Priya Parekh

Some aquatic invertebrates, such as *Artemia franciscana,* produce dormant cysts that remain viable out of water for long periods of time. These cysts are the main dispersal stage for the species, and their dispersal is believed to be caused, at least in part, by passive vectors such as wind. The objectives of this

study were to determine the minimum wind speed required for *A. franciscana* cysts to disperse and the frequency of dispersal events. The relationship between wind speed and dispersal was investigated in Lac du Bois Grasslands Park north of Kamloops, B.C., where *A. franciscana* naturally occurs, and in the laboratory using a wind tunnel. In Lac du Bois Park, wind speed requirement for dispersal was assessed by completing seven replicate dispersal trials in which trays with *A. franciscana* cysts were placed at an exposed and a sheltered site for two hours, and then number of cysts remaining were counted. Field anemometers continuously monitored wind speed at each site during the study. Within the wind tunnel, wind speed was regulated during five dispersal trials to log the number of cysts dispersed at particular wind speeds recorded at ground surface. Dispersal data from the field and from the wind tunnel revealed a threshold for 50% dispersal at 13 km/h; dispersal then increased at higher wind speeds up to a plateau of 90-100% dispersal at≥23 km/h. Historical wind speed data from the Kamloops airport and the results for wind speed requirement for dispersal were then utilized to predict how often dispersal events occurred per year in Lac du Bois Park from 1967 to 2011.

Eldorado Gold Project: Statistical Comparison of ICP-AES and XRF Analysis in Mineral Exploration

Student: Katelyn Pocha
Supervisor: John Greenough

The Eldorado Gold project, a mesothermal to epithermal orogenic gold system, is located in the Chilcotin ranges of the south central interior of British Columbia. During the summer of 2011, an exploration program was conducted that included the geochemical analysis of soil samples using Inductively Coupled Plasma – Atomic Emission Spectroscopy (ICP-AES) and X-ray Fluorescence (XRF). Due to the fast pace of the exploration program, the XRF data was relied upon for inferring anomalous gold using arsenic as a 'pathfinder'. This study statistically analyzes the two analytical techniques to determine if XRF is reliable in early stage exploration programs when compared to ICP-AES. Analysis shows that elements with low XRF detection limits (specifically arsenic, copper, iron, titanium and zinc) have high correlations with the ICP data, and elements with high XRF detection limits have low correlations. To further the study of XRF and ICP-AES relationships, stepwise multiple regression techniques were used for each analytical technique to hypothesize elemental combinations that could better predict gold anomalies. This exercise examines whether or not the optimal multiple regression equation uses the same elements regardless of XRF or ICP-AES analysis. Not surprisingly, the ICP-AES data leads to a better estimate; the standard error of estimate for ICP-AES is 0.3916 whereas for XRF data it is 0.4203. When taking analytical costs and the immediate need for data into account, XRF analysis is a reliable analytical technique.

The Importance of Human-Nature Interaction: Applications to Our Built Environments

Student: Matei Rau
Supervisor: Paul Davies

The purpose of this presentation is to provide an overview of how inclusion of natural elements into built environments can affect the psychological state of the humans interacting within the space. Throughout history, humans have relied on their natural habitats for shelter and survival. A number of environmental psychology theories state that we are intrinsically drawn to nature more so than to urban settings. Such theories also express that there are a variety of psychological benefits to human-nature interaction. A large portion of past architecture has treated our built habitats as being independent from the natural environment on which they are built. This way of thinking has overlooked the possible negative consequences that are related to our daily separation from the natural environment. More recently, a shift in architectural thinking has accepted the need for unity between built environments and the natural world. This new view accepts the theories presented by environmental psychologists and recognizes the psychological benefits of human-nature interaction. This presentation will examine a number of positive consequences associated with the inclusion of various natural elements into built environments. Furthermore, we will examine some of the ways in which architects are currently implementing such elements into newly built architectural works.

Cloning a Putative Hemolysin Gene from *Vibrio fisheri*

Student: Ben Robinson
Supervisor: Steve Thomas
Department of Biology, UFV, Abbotsford BC

My project involves the cloning and expression of a putative hemolysin gene within *Vibrio fischeri* species MJ1. A previous project supervised by Stephen Thomas involved the cloning and sequencing of a region downstream of the *lux* operon responsible for glowing phenotype of *V. fischeri* in search of a *rib* operon. What they found instead was the beginnings of a putative hemolysin gene. My task is to isolate this gene in its entirety using PCR and inserting it into pGEM, followed by transformation into DH5 alpha E.coli cells. Expression can be screened by observing hemolysis on blood agar plates. The interest of this experiment stems from the potential toxicity of this seemingly harmless bacterial species that lives in symbiosis with several marine organisms. If *V. fischeri* contains a hemolysin gene, future research could look into regulation of this potentially harmful toxin. So far, DNA has been successfully extracted from *V. fischeri* and a PCR product the size of the putative hemolysin gene has been obtained using primers I have designed that flank the gene. The PCR product and pGEM was digested with BAMH1 and EcoR1 and currently I am preparing for ligation. The next step is transformation of pGEM with insert into DH5alpha cells followed by blood agar screening.

Metabolomic Examination of *Streptomyces* species Using Nuclear Magnetic Resonance Spectroscopy and Multivariate Statistical Analysis.

Student: Derek Rollo
Supervisor: Dr. Paul Shipley

Streptomyces is a soil-inhabiting genus of Gram-positive aerobic bacteria of family streptomycetaceae, order actinomycetales and class acinobacteria. *Streptomyces* spp. contributes about two thirds of all microbially produced antibiotics due to their extensive secondary metabolism. Different spp. produce relatively unique secondary metabolites that are bioactive as antibiotic, antifungal, insecticidal, anti-neoplastic, anti-parasitic, and immunosuppressant drugs. Two-dimensional J-resolved nuclear magnetic resonance (NMR) spectroscopy can be coupled with principal component analysis (PCA) and partial least squares discriminant analysis (PLS-DA) to facilitate metabolomic examination of different spp. This approach was applied for the examination of ethyl acetate extractions of cultured *S. laurentii*, *S. nodosus*, *S. coelicolor*, *S. parvulus* and one unknown species. Principal components were computed to represent variance within the sample groups. Interpretation of the PCA and PLS-DA statistical models resulting from processed NMR data allowed for a comparison of similarities and differences between the *Streptomyces* spp. Loadings plots were examined in order to identify peaks that contributed to variance in the models. These were then compared to known bioactive secondary metabolites to determine if they had a significant impact on the observed variance. Additional sources of variance, which were not readily identifiable, were examined to determine if they might be unknown compounds that could represent novel secondary metabolites. NMR coupled with MVA is intrinsically useful for chemotaxonomic purposes. Furthermore, it allows a method for screening unique compounds from newly discovered *Streptomyces* spp., promoting the discovery of putative bioactive metabolites.

Using Operant Conditioning to Facilitate Physiological Sampling from Captive Ungulates

Student: Jillian Rutherford
Supervisor: Dr. John Church

Captive animals are often subjected to stressful procedures in order for physiological data to be procured. These methods can be dangerous, ineffective, and have negative impacts on the welfare of both the animals and handlers involved. Novel sampling techniques such as saliva analysis and thermographic imaging have been developed as viable alternatives to stressful forms of conventional veterinary medicine. The goal of this study was to determine if individuals from several captive ungulate species could be trained to willingly provide saliva samples and thermographic images, as alternatives to traditional sampling practices. Behavioural modification through operant conditioning was applied to members of the Elk, Camel, and Bighorn Sheep herds at the BC Wildlife Park. Both sample-providing behaviours were successfully trained in all three species, facilitating the collection of the respective data sets. This cooperative approach to veterinary action improves access to the health profiles of these individuals while minimizing stress and pain. The combination of novel sampling techniques and

behavioural modification through operant conditioning can allow regular health monitoring and earlier diagnosis of illness, leading to greater overall wellbeing of captive ungulates.

Deerhorn Geochemistry and Cu-Au Mineral Paragenesis: Woodjam Porphyry Cu-Au District, British Columbia, Canada

Student: Julia Scott
Supervisor: Dr. John Greenough

The Deerhorn prospect occurs in the Woodjam Cu-Au Porphyry in central British Columbia's Cariboo Mining district and within the Quesnellia Terrane. Woodjam is comprised of successive Triassic-Jurassic Nicola Group volcaniclastic rocks intruded by the late Triassic-early Jurassic Takomkane Batholith in the southern portion of the property. Mineralisation is genetically related to, ca. 197 Ma, moderately dipping (25^0) north, mudstone to sandstone volcanic-sedimentary host rock, overlain by unmineralised andesite lavas. Several monzonitic dykes intrude the host stratigraphy and both early (pre-mineralisation = Monzonite A) and late (post-mineralisation = Monzonite D) facies are recognised. Two drill holes from the Deerhorn target area are studied. Five vein types are identified and classified into four stages of formation in drill hole DH11-32 and four vein types are identified and classified in DH09-03. Early-stage veins include magnetite stringers (DH11-32) and hematite – chlorite ± pyrite (DH09-03) veins, associated with the Volcanic Sandstone mineralised host rock. Both drill holes have main mineralised stage veins with quartz – chlorite - ± magnetite ± hematite – pyrite – chalcopyrite ± bornite ± chalcocite ± covellite mineral assemblages, with pervasive potassic and magnetite – hematite alteration occurring in Volcanic Sandstone and Monzonite A. Late stage veins are associated with propylitic and phyllic alteration in vein mineral assemblages of sericite – chlorite – pyrite – epidote ± hematite ± magnetite ± hornblende ± tourmaline in Monzonite D and plagioclase porphyritic andesite. Lastly, post – mineralisation carbonate and fluidal hydrothermal veins cut all lithologies. Geochemical and petrographic data sets are combined and simultaneously examined with multidimensional scaling (MDS) to reveal relationships between mineral abundances and element concentrations. MDS diagrams suggest that magnetite abundance, as opposed to hematite percentage, is correlated with gold, copper, chalcopyrite, bornite, and chalcocite mineralisation. Apparently magnetite enrichment is associated with economic mineralisation.

Testing Scheme for the Detection of MAP Bacteria in Bovine Fecal Samples

Student: Sneha Thomas
Supervisor: Terry Starr
Department of Biology, UFV, Abbotsford BC

Mycobacterium avium subspecies paratuberculosis (MAP) is a causative agent in Johne's disease, which is a gastrointestinal, chronic wasting disorder that affects bovine species. It is a gram positive bacillus

bacterium, capable of surviving the process of pasteurization. Additionally, detectable growth of the bacteria, within an infected animal, is only generally seen in the latter stages of the disease. Thus, MAP is a slow growing bacterium that can take up to six months for noticeable growth on a solid media. The purpose of this project was to develop a testing scheme that allowed for the rapid growth and detection of MAP in bovine feces, particularly using liquid media. The fecal samples were both fresh and frozen. Samples were cultured and stained using both acid-fast and fluorescent staining techniques. Positive growth was to be further confirmed with PCR using the HSPX primers. HSPX is a heat shock protein that is highly specific to MAP. Interestingly, it was found that significant growth was seen on the solid media within 3 weeks; some growth was also seen from the liquid media. The positive samples are to be confirmed with PCR and the results are to be obtained. Further analysis and data collection is needed for a conclusive discussion.

Identification of indigenous diesel degrading bacteria from contaminated soil and subsequent study of genes responsible for hydrocarbon metabolism

Student: James VanderHorst, University of the Fraser Valley
Supervisor: Steven Thomas

Due to its extensive use, hydrocarbons constitute a large portion of the contaminants present in the environment today. Bioremediation is a process which makes use of the ability of certain microorganisms to degrade contaminants in specific environments. A local contaminated soil site was analyzed for the presence of bacteria which have the ability to metabolize diesel. After isolation using Bushnell Haas media which selected for diesel degradation, physiological and genetic methods were used to identify the genus of the species found in the soil site. 16S rRNA sequencing analysis used in conjunction with BLAST database searches confirmed the presence of rhodococcus and gordonia bacterium. Upon identification, directed research was done on the alkane hydroxylase systems in place in these bacteria, which are involved with diesel degradation. Future research should be directed to the specific alkB genes involved in the alkane hydroxlase system in order to intensify the efficiency of the bacteria already used in bioremediation procedures.

Determination of the Thermal Conductivity of Lakebed and Streambed Materials Using a Thermal Probe

Student: Jordan White
Supervisor: Dr. Craig Nichol

Groundwater discharge occurs when the water table reaches the surface at lakes and streams. Using the velocity of the groundwater flow, the volume of groundwater entering a lake or stream can be calculated. An alternative to physical measurements, such as seepage meters, relies on the principle of heat transfer. As groundwater enters a lake or stream, the water carries heat with it. The heat flow can be simulated using a computer model in order to generate an estimate of the groundwater discharge. This method is non-obtrusive, environmentally friendly, provides a constant source of analyzable data, does not introduce contamination by chemical tracers, and provides quick field-obtainable data that does not require laboratory analysis. Thermal conductivity of the sediment is an important parameter, as sediment grain size and hence thermal conductivity varies throughout the lake. In-situ measurements of thermal conductivity can increase accuracy of the calculated groundwater velocity. A new probe design for measuring the in-situ thermal conductivity has been developed. The probe uses Type T thermocouples potted with thermally conductive epoxy inside of a central structural tube. The heating element consists of a NiChrome wire wrapped around the inner support tube, and heating is controlled by a constant current driver connected to a 24-volt power supply. The heater assembly is potted in an outer aluminum casing tube designed to be driven into sediment. Natural temperature profiles are first collected, followed by a heat pulse that can trace the dissipation of heat into the sediments. The probe was calibrated and tested in the laboratory with different sediments of known thermal conductivity, and will be tested in the field.

Computational Evaluations of Adenosyl Group Rotations in Adenosylcobalamin

Student: Gordon Wong
Supervisor: Dr. David Jack

Adenosylcobalamin (AdoCbl) is one of the most complex organometallic cofactors found in nature in terms of its molecular weight and reaction mechanism. AdoCbl-dependent enzymes catalyze a complex array of radical-mediated isomerization reactions. The catalytic cycle is initiated by homolytic cleavage of the organometallic bond between Co and C5' of the corrin ring and adenosyl moiety, respectively. Due to the highly reactive nature of its radical components, a key control issue for AdoCbl-dependent enzymes is unintended initiation of the catalytic cycle. To circumvent this problem, AdoCbl-dependent enzymes tightly regulate their Co-C bond homolysis equilibriums. However, determining the mechanism by which these enzymes are able to regulate homolysis, via labilization of the Co-C bond, is the most enduring problem of coenzyme B_{12} biochemistry. Interestingly, in almost all crystal structures of AdoCbl-dependent enzymes, this Co-C bond is ruptured. However, $_D$-Ornithine 4,5-aminomutase (OAM) is the only enzyme where this bond is found intact. In addition, OAM also imposes a unique placement on its

adenosyl group with respect to the corrin ring. To elucidate the electrostatic effects of this novel conformation we employed computational methods. We specifically chose GAMESS, an *ab initio* quantum mechanical computer-simulation program that can utilize density-functional theory approximations, to examine this system. We first subjected AdoCbl to geometry optimizations in a vacuum environment. Subsequently, we performed calculations to gather information about local energy minima, charge distributions, and Co-C bond energies associated with various adenosyl placements. In particular, the energies and geometries of various placements of the adenosyl group over the A and B sites (sub-rings) of the corrin ring were determined and their implications for Co-C5' bond stability examined.

Sample Matrix Interferences in Analytical Methods for the Detection and Quantification of BMAA

Student: Broc Glover

N-β-methylamino-L-alanine, or BMAA, is a non-protein amino acid produced by cyanobacteria and biomagnified in food chains.   A link has been established between BMAA and several progressive neurodegenerative diseases and BMAA has been found in autopsy samples of patients who died of Alzheimer's, Amyotrophic Lateral Sclerosis (ALS) and ALS-Parkinson Dementia Complex. Recent evidence has demonstrated that BMAA can be misincorporated into brain proteins through an error in translation resulting in protein misfolding and precipitation. Such a mechanism may explain protein aggregation and plaque development that characterizes neurodegenerative disease. However, the research is still controversial and several labs have reported conflicting findings with respect to the identification and quantification of BMAA. A crucial component of further research is the development of reliable methods for a wide range of sample matrices. Investigated here is the impact of matrix affects on both the detection and quantification of BMAA by liquid chromatography coupled to fluorescence detection and time of flight mass spectrometry. Specifically, we report that BMAA readily forms metal adducts with sodium, magnesium, copper and zinc that complicate mass spectra by changing the mass to charge ratio and masking the BMAA signal. A dimer of the BMAA molecule and metal-BMAA-dimer complexes have also been frequently observed in the samples. Therefore, many of the researchers who have reported quantification by only a parent ion by electrospray ionization have reported false negative findings. Further, we also show that by using three different instruments, with three different detection methods, we produced highly variable results, demonstrating that additional work is required for development of an optimized, rugged method for broad application.

Food and Water Security – Sustainably Feeding the World

Student: Joanne Taylor
Supervisor: John Wagner

Never before has the concept of food and water security been more urgent than in the 21st century. Starvation and poverty have become pervasive in every area of the globe affecting the majority of people living in densely populated areas (UNFAO 2009). Inextricably tied to this problem is burgeoning population growth especially in the global south (Beuchelt et al. 2012). Climate change is affecting rainfall and increasing extreme weather patterns that severely alter who are getting water, and therefore food (Chartres et al. 2011). The urgency of this dilemma requires immediate global attention. The question to be asked is how water productivity can be increased with the efficient use of irrigation systems together with the improved use of rain water, supplemented with local, small agricultural systems that involve farmers and farming organizations. Cuba is the only country in the world that has successfully adopted a self-reliant method of feeding its population that does not rely on petro-chemicals, land greedy, mono-culture food production, and the exploitation of un-sustainable groundwater extraction that simultaneously increases water and soil pollution with agro-chemicals (Hiranandani 2009). California also offers innovative and alternative methods of capturing rainwater and innovative agricultural methods that that can offer solutions to the future of water sustainability (Schulte 2012, Gleick 2003). This paper suggests that the Cuban and California models are a viable and environmentally plausible solution to the water–food security problem.

A Metabolomic Analysis of Hawthorn (*Crataegus* spp.) using NMR and Multivariate Statistics

Student: Cynthia Shum
Supervisor: Dr. Paul Shipley

Hawthorn, *Crataegus* spp. is commonly used in natural health products for preventing and treating cardiovascular diseases. Fruits, leaves and berries of hawthorn are considered the most potent parts of the plant. Phenolic compounds derived from hawthorn are thought to contribute significantly to its therapeutic effects. These include hyperoside, isoquercitrin, chlorogenic acid, ideain, epicatechin and procyanidin polymers. The methanolic leaf extracts of *Crataegus wilsonii*, *C. almaatensis*, *C. maximowiczii*, *C. hupehensis*, *C. pinnatifidia*, *C. heldreichii, C. monogyna* and *C. hypehensis* were analyzed using 2D J-resolved nuclear magnetic resonance spectroscopy coupled with multivariate statistical analysis (MVA). This allowed for determining the sources of variance between species based on whole leaf metabolome and phenolic compound composition.

Through examination of loadings plots we found the separation of samples observed in principal component analysis (PCA) scatter plots was mainly influenced by variance in concentrations of olefinic C18 fatty acids. Analysis of the phenolics/aromatics region in the *Crataegus* spp. revealed that the observed variance was greatly influenced by chlorogenic acid and the flavonoid vitexin-2"-O-rhamnoside. Partial least-squares discriminant analysis (PLS-DA) identified important chemical shifts

responsible for differentiation between the seven species. Models produced variable importance lists where the relationship between the species was greatly influenced by olefinic C18 fatty acids, consistent with the results obtained through PCA. The variance within the phenolics/aromatics region seen in PCA was also observed in PLS-DA, where variance was determined by vitexin-2"-O-rhamnoside. Cross-validation of the models yielded predictability scores, Q^2, within $0.863 - 0.978$, suggesting that the models created were valid.